

## SEQUENCE LISTING

&lt;110&gt; BASF Plant Science GmbH

&lt;120&gt; Verfahren zur Herstellung von mehrfach ungesättigten Fettsäuren in transgenen Organismen

&lt;130&gt; PF54756

&lt;140&gt; 20030601

&lt;141&gt; 2003-08-01

&lt;160&gt; 192

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 1266

&lt;212&gt; DNA

&lt;213&gt; Euglena gracilis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1266)

&lt;223&gt; Delta-8-Desaturase

&lt;400&gt; 1

atg aag tca aag cgc caa gcg ctt ccc ctt aca att gat gga aca aca	48
Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr	
1 5 10 15	

tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att	96
Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile	
20 25 30	

ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg	144
Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met	
35 40 45	

cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat	192
His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn	
50 55 60	

ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag	240
Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu	
65 70 75 80	

gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat	288
Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp	
85 90 95	

gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt	336
Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu	
100 105 110	

gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att	384
Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile	
115 120 125	

ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct	432
Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser	
130 135 140	

cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac	480
His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn	
145 150 155 160	

[illegible]

<210> 2  
 <211> 421  
 <212> PRT  
 <213> *Euglena gracilis*

<400> 2

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Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile  
 20 25 30

Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met  
 35 40 45

His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn  
 50 55 60

Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu  
 65 70 75 80

Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp  
 85 90 95

Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu  
 100 105 110

Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile  
 115 120 125

Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser  
 130 135 140

His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn  
 145 150 155 160

Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr  
 165 170 175

Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln  
 180 185 190

Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu  
 195 200 205

Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe  
 210 215 220

Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp  
 225 230 235 240

4

Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn  
 245 250 255  
 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu  
 260 265 270  
 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile  
 275 280 285  
 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe  
 290 295 300  
 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile  
 305 310 315 320  
 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His  
 325 330 335  
 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly  
 340 345 350  
 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg  
 355 360 365  
 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys  
 370 375 380  
 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile  
 385 390 395 400  
 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro  
 405 410 415  
 Ala Gly Lys Ala Leu  
 420

<210> 3  
 <211> 777  
 <212> DNA  
 <213> Isochrysis galbana  
 <220>  
 <221> CDS  
 <222> (1)..(777)  
 <223> Delta-9-Elongase

<400> 3  
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 Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr  
 1 5 10 15  
 gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg 96  
 Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro  
 20 25 30

## 5

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg 144  
 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg  
 35 40 45

acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg 192  
 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu  
 50 55 60

agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc 240  
 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly  
 65 70 75 80

gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag 288  
 Ala Trp Leu Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln  
 85 90 95

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag 336  
 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys  
 100 105 110

gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg 384  
 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu  
 115 120 125

agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat 432  
 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp  
 130 135 140

gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg 480  
 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met  
 145 150 155 160

ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc 528  
 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu  
 165 170 175

acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg 576  
 Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met  
 180 185 190

cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc 624  
 Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile  
 195 200 205

aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct 672  
 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala  
 210 215 220

ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt 720  
 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe  
 225 230 235 240

ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag 768  
 Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys  
 245 250 255

cag ctc tag 777  
 Gln Leu

&lt;210&gt; 4

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Isochrysis galbana

&lt;400&gt; 4

Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr  
 1 5 10 15  
 Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro  
 20 25 30  
 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg  
 35 40 45  
 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu  
 50 55 60  
 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly  
 65 70 75 80  
 Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln  
 85 90 95  
 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys  
 100 105 110  
 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu  
 115 120 125  
 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp  
 130 135 140  
 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met  
 145 150 155 160  
 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu  
 165 170 175  
 Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met  
 180 185 190  
 Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile  
 195 200 205  
 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala  
 210 215 220  
 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe  
 225 230 235 240  
 Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys  
 245 250 255  
 Gln Leu

<210> 5  
 <211> 1410  
 <212> DNA  
 <213> *Phaeodactylum tricornutum*

<220>  
 <221> CDS  
 <222> (1)..(1410)  
 <223> Delta-5-Desaturase

<400> 5  
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 Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val  
 1 5 10 15  
 gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt 96  
 Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser  
 20 25 30  
 ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat 144  
 Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr  
 35 40 45  
 gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt 192  
 Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe  
 50 55 60  
 ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat 240  
 Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His  
 65 70 75 80  
 acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gtg acg gat 288  
 Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp  
 85 90 95  
 ttc gtc tgc gag tac aag ttc gat acc gaa ttt gaa cgc gaa atc aaa 336  
 Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys  
 100 105 110  
 cga gaa gtc ttc aag att gtg cga cga ggc aag gat ttc ggt act ttg 384  
 Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu  
 115 120 125  
 gga tgg ttc ttc cgt gcg ttt tgc tac att gcc att ttc ttc tac ctg 432  
 Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu  
 130 135 140  
 cag tac cat tgg gtc acc acg gga acc tct tgg ctg ctg gcc gtg gcc 480  
 Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala  
 145 150 155 160  
 tac gga atc tcc caa gcg atg att ggc atg aat gtc cag cac gat gcc 528  
 Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala  
 165 170 175  
 aac cac ggg gcc acc tcc aag cgt ccc tgg gtc aac gac atg cta ggc 576  
 Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly  
 180 185 190  
 ctc ggt gcg gat ttt att ggt ggt tcc aag tgg ctg tgg cag gaa caa 624  
 Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln  
 195 200 205  
 cac tgg acc cac cac gct tac acc aat cac gcc gag atg gat ccc gat 672  
 His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp  
 210 215 220

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agc ttt ggt gcc gaa cca atg ctc cta ttc aac gac tat ccc ttg gat      720
Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp
225                      230                      235                      240

cat ccc gct cgt acc tgg cta cat cgc ttt caa gca ttc ttt tac atg      768
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met
245                      250                      255

ccc gtc ttg gct gga tac tgg ttg tcc gct gtc ttc aat cca caa att      816
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile
260                      265                      270

ctt gac ctc cag caa cgc ggc gca ctt tcc gtc ggt atc cgt ctc gac      864
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp
275                      280                      285

aac gct ttc att cac tcg cga cgc aag tat gcg gtt ttc tgg cgg gct      912
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala
290                      295                      300

gtg tac att gcg gtg aac gtg att gct ccg ttt tac aca aac tcc ggc      960
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly
305                      310                      315                      320

ctc gaa tgg tcc tgg cgt gtc ttt gga aac atc atg ctc atg ggt gtg      1008
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val
325                      330                      335

gcg gaa tcg ctc gcg ctg gcg gtc ctg ttt tcg ttg tcg cac aat ttc      1056
Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe
340                      345                      350

gaa tcc gcg gat cgc gat ccg acc gcc cca ctg aaa aag acg gga gaa      1104
Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu
355                      360                      365

cca gtc gac tgg ttc aag aca cag gtc gaa act tcc tgc act tac ggt      1152
Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly
370                      375                      380

gga ttc ctt tcc ggt tgc ttc acg gga ggt ctc aac ttt cag gtt gaa      1200
Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu
385                      390                      395                      400

cac cac ttg ttc cca cgc atg agc agc gct tgg tat ccc tac att gcc      1248
His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala
405                      410                      415

ccc aag gtc cgc gaa att tgc gcc aaa cac gcc gtc cac tac gcc tac      1296
Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr
420                      425                      430

tac ccg tgg atc cac caa aac ttt ctc tcc acc gtc cgc tac atg cac      1344
Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His
435                      440                      445

gcg gcc ggg acc ggt gcc aac tgg cgc cag atg gcc aga gaa aat ccc      1392
Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro
450                      455                      460

ttg acc gga cgg gcg taa
Leu Thr Gly Arg Ala
465

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<210> 6  
<211> 469  
<212> PRT



&lt;213&gt; Phaeodactylum tricornutum

&lt;400&gt; 6

Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val  
 1 5 10 15

Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser  
 20 25 30

Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr  
 35 40 45

Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe  
 50 55 60

Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His  
 65 70 75 80

Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp  
 85 90 95

Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys  
 100 105 110

Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu  
 115 120 125

Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu  
 130 135 140

Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala  
 145 150 155 160

Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala  
 165 170 175

Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly  
 180 185 190

Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln  
 195 200 205

His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp  
 210 215 220

Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp  
 225 230 235 240

His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met  
 245 250 255

Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile  
 260 265 270

Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp  
 275 280 285

Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala  
 290 295 300

Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly  
 305 310 315 320

Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val  
 325 330 335

Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe  
 340 345 350

Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu  
 355 360 365

Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly  
 370 375 380

Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu  
 385 390 395 400

His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala  
 405 410 415

Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr  
 420 425 430

Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His  
 435 440 445

Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro  
 450 455 460

Leu Thr Gly Arg Ala  
 465

<210> 7  
 <211> 1344  
 <212> DNA  
 <213> *Ceratodon purpureus*

<220>  
 <221> CDS  
 <222> (1)..(1344)  
 <223> Delta-5-Desaturase

<400> 7

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Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp	
1 5 10 15	
gga aaa tgg tgt caa att gac gat gct gtc ctg aga tca cat cca ggt	96
Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly	
20 25 30	
ggt agt gca att act acc tat aaa aat atg gat gcc act acc gta ttc	144
Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe	
35 40 45	
cac aca ttc cat act ggt tct aaa gaa gcg tat caa tgg ctg aca gaa	192
His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu	
50 55 60	
ttg aaa aaa gag tgc cct aca caa gaa cca gag atc cca gat att aag	240
Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys	
65 70 75 80	
gat gac cca atc aaa gga att gat gat gtg aac atg gga act ttc aat	288
Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn	
85 90 95	
att tct gag aaa cga tct gcc caa ata aat aaa agt ttc act gat cta	336
Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu	
100 105 110	
cgt atg cga gtt cgt gca gaa gga ctt atg gat gga tct cct ttg ttc	384
Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe	
115 120 125	
tac att aga aaa att ctt gaa aca atc ttc aca att ctt ttt gca ttc	432
Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe	
130 135 140	
tac ctt caa tac cac aca tat tat ctt cca tca gct att cta atg gga	480
Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly	
145 150 155 160	
gtt gcg tgg caa caa ttg gga tgg tta atc cat gaa ttc gca cat cat	528
Val Ala Trp Gln Leu Glu Gly Trp Leu Ile His Glu Phe Ala His His	
165 170 175	
cag ttg ttc aaa aac aga tac tac aat gat ttg gcc agc tat ttc gtt	576
Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val	
180 185 190	
gga aac ttt tta caa gga ttc tca tct ggt ggt tgg aaa gag cag cac	624
Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His	
195 200 205	
aat gtg cat cac gca gcc aca aat gtt gtt gga cga gac gga gat ctt	672
Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu	
210 215 220	
gat tta gtc cca ttc tat gct aca gtg gca gaa cat ctc aac aat tat	720
Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr	
225 230 235 240	
tct cag gat tca tgg gtt atg act cta ttc aga tgg caa cat gtt cat	768
Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His	
245 250 255	
tgg aca ttc atg tta cca ttc ctc cgt ctc tcg tgg ctt ctt cag tca	816
Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser	
260 265 270	

atc att ttt gtt agt cag atg cca act cat tat tat gac tat tac aga 864  
 Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg.  
 275 280 285

aat act gcg att tat gaa cag gtt ggt ctc tct ttg cac tgg gct tgg 912  
 Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp  
 290 295 300

tca ttg ggt caa ttg tat ttc cta ccc gat tgg tca act aga ata atg 960  
 Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met  
 305 310 315 320

ttc ttc ctt gtt tct cat ctt gtt gga ggt ttc ctg ctc tct cat gta 1008  
 Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val  
 325 330 335

gtt act ttc aat cat tat tca gtg gag aag ttt gca ttg agc tcg aac 1056  
 Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn  
 340 345 350

atc atg tca aat tac gct tgt ctt caa atc atg acc aca aga aat atg 1104  
 Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met  
 355 360 365

aga cct gga aga ttc att gac tgg ctt tgg gga ggt ctt aac tat cag 1152  
 Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln  
 370 375 380

att gag cac cat ctt ttc cca acg atg cca cga cac aac ttg aac act 1200  
 Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr  
 385 390 395 400

gtt atg cca ctt gtt aag gag ttt gca gca gca aat ggt tta cca tac 1248  
 Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr  
 405 410 415

atg gtc gac gat tat ttc aca gga ttc tgg ctt gaa att gag caa ttc 1296  
 Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe  
 420 425 430

cga aat att gca aat gtt gct gct aaa ttg act aaa aag att gcc tag 1344  
 Arg Asn Ile Ala Asn Val Ala Lys Leu Thr Lys Lys Ile Ala  
 435 440 445

<210> 8  
 <211> 447  
 <212> PRT  
 <213> Ceratodon purpureus

<400> 8

Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp  
 1 5 10 15

Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly  
 20 25 30

Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe  
 35 40 45

His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu  
 50 55 60

## 13

Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys  
 65 70 75 80

Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn  
 85 90 95

Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu  
 100 105 110

Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe  
 115 120 125

Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe  
 130 135 140

Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly  
 145 150 155 160

Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His  
 165 170 175

Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val  
 180 185 190

Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His  
 195 200 205

Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu  
 210 215 220

Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr  
 225 230 235 240

Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His  
 245 250 255

Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser  
 260 265 270

Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg  
 275 280 285

Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp  
 290 295 300

Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met  
 305 310 315 320

Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val  
 325 330 335

14

Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn  
340 345 350

Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met  
355 360 365

Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln  
370 375 380

Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr  
385 390 395 400

Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr  
405 410 415

Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe  
420 425 430

Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala  
435 440 445

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<211> 1443  
<212> DNA  
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Met Ala Pro His Ser Ala Asp Thr Ala Gly Leu Val Pro Ser Asp Glu  
1 5 10 15  
ttg agg cta cga acg tcg aat tca aag ggt ccc gaa caa gag caa act 96  
Leu Arg Leu Arg Thr Ser Asn Ser Lys Gly Pro Glu Gln Glu Gln Thr  
20 25 30  
ttg aag aag tac acc ctt gaa gat gtc agc cgc cac aac acc cca gca 144  
Leu Lys Lys Tyr Thr Leu Glu Asp Val Ser Arg His Asn Thr Pro Ala  
35 40 45  
gat tgt tgg ttg gtg ata tgg ggc aaa gtc tac gat gtc aca agc tgg 192  
Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp  
50 55 60  
att ccc aat cat ccg ggg ggc agt ctc atc cac gta aaa gca ggg cag 240  
Ile Pro Asn His Pro Gly Gly Ser Leu Ile His Val Lys Ala Gly Gln  
65 70 75 80  
gat tcc act cag ctt ttc gat tcc tat cac ccc ctt tat gtc agg aaa 288  
Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys  
85 90 95  
atg ctc gcg aag tac tgt att ggg gaa tta gta ccg tct gct ggt gat 336  
Met Leu Ala Lys Tyr Cys Ile Gly Glu Leu Val Pro Ser Ala Gly Asp  
100 105 110

## 15

gac aag ttt aag aaa gca act ctg gag tat gca gat gcc gaa aat gaa Asp Lys Phe Lys Lys Ala Thr Leu Glu Tyr Ala Asp Ala Glu Asn Glu 115 120 125	384
gat ttc tat ttg gtt gtg aag caa cga gtt gaa tct tat ttc aag agt Asp Phe Tyr Leu Val Val Lys Gln Arg Val Glu Ser Tyr Phe Lys Ser 130 135 140	432
aac aag ata aac ccc caa att cat cca cat atg atc ctg aag tca ttg Asn Lys Ile Asn Pro Gln Ile His Pro His Met Ile Leu Lys Ser Leu 145 150 155 160	480
ttc att ctt ggg gga tat ttc gcc agt tac tat tta gcg ttc ttc tgg Phe Ile Leu Gly Tyr Phe Ala Ser Tyr Tyr Leu Ala Phe Phe Trp 165 170 175	528
tct tca agt gtc ctt gtt tct ttg ttt ttc gca ttg tgg atg ggg ttc Ser Ser Ser Val Leu Val Ser Leu Phe Phe Ala Leu Trp Met Gly Phe 180 185 190	576
ttc gca gcg gaa gtc ggc gtg tcg att caa cat gat gga aat cat ggt Phe Ala Ala Glu Val Gly Val Ser Ile Gln His Asp Gly Asn His Gly 195 200 205	624
tca tac act aaa tgg cgt ggc ttt gga tat atc atg gga gcc tcc cta Ser Tyr Thr Lys Trp Arg Gly Phe Gly Tyr Ile Met Gly Ala Ser Leu 210 215 220	672
gat cta gtc gga gcc agt agc ttc atg tgg aga cag caa cac gtt gtg Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Val 225 230 235 240	720
gga cat cac tcg ttt aca aat gtg gac aac tac gat cct gat att cgt Gly His His Ser Phe Thr Asn Val Asp Asn Tyr Asp Pro Asp Ile Arg 245 250 255	768
gtg aaa gat cca gat gtc agg agg gtt gcg acc aca caa cca aga caa Val Lys Asp Pro Asp Val Arg Arg Val Ala Thr Thr Gln Pro Arg Gln 260 265 270	816
tgg tat cat gcg tat cag cat atc tac ctg gca gta tta tat gga act Trp Tyr His Ala Tyr Gln His Ile Tyr Leu Ala Val Leu Tyr Gly Thr 275 280 285	864
cta gct ctt aag agt att ttt cta gat gat ttc ctt gcg tac ttc aca Leu Ala Leu Lys Ser Ile Phe Leu Asp Asp Phe Leu Ala Tyr Phe Thr 290 295 300	912
gga tca att ggc cct gtc aag gtg gcg aaa atg acc ccc ctg gag ttc Gly Ser Ile Gly Pro Val Lys Val Ala Lys Met Thr Pro Leu Glu Phe 305 310 315 320	960
aac atc ttc ttt cag gga aag ctg cta tat gcg ttc tac atg ttc gtg Asn Ile Phe Phe Gln Gly Lys Leu Leu Tyr Ala Phe Tyr Met Phe Val 325 330 335	1008
ttg cca tct gtg tac ggt gtt cac tcc gga gga act ttc ttg gca cta Leu Pro Ser Val Tyr Gly Val His Ser Gly Gly Thr Phe Leu Ala Leu 340 345 350	1056
tat gtg gct tct cag ctc att aca ggt tgg atg tta gct ttt ctt ttt Tyr Val Ala Ser Gln Leu Ile Thr Gly Trp Met Leu Ala Phe Leu Phe 355 360 365	1104
caa gta gca cat gtc gtg gat gat gtt gca ttt cct aca cca gaa ggt Gln Val Ala His Val Val Asp Asp Val Ala Phe Pro Thr Pro Glu Gly 370 375 380	1152

ggg aag gtg aag gga gga tgg gct gca atg cag gtt gca aca act acg 1200  
 Gly Lys Val Lys Gly Gly Trp Ala Ala Met Gln Val Ala Thr Thr Thr  
 385 390 395 400  
 gat ttc agt cca cgc tca tgg ttc tgg ggt cat gtc tct gga gga tta 1248  
 Asp Phe Ser Pro Arg Ser Trp Phe Trp Gly His Val Ser Gly Gly Leu  
 405 410 415  
 aac aac caa att gag cat cat ctg ttt cca gga gtg tgc cat gtt cat 1296  
 Asn Asn Gln Ile Glu His His Leu Phe Pro Gly Val Cys His Val His  
 420 425 430  
 tat cca gcc att cag cct att gtc gag aag acg tgc aag gaa ttc gat 1344  
 Tyr Pro Ala Ile Gln Pro Ile Val Glu Lys Thr Cys Lys Glu Phe Asp  
 435 440 445  
 gtg cct tat gta gcc tac cca act ttt tgg act gcg ttg aga gcc cac 1392  
 Val Pro Tyr Val Ala Tyr Pro Thr Phe Trp Thr Ala Leu Arg Ala His  
 450 455 460  
 ttt gcg cat ttg aaa aag gtt gga ttg aca gag ttt cgg ctc gat ggc 1440  
 Phe Ala His Leu Lys Lys Val Gly Leu Thr Glu Phe Arg Leu Asp Gly  
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 <213> Physcomitrella patens

<400> 10

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20 25 30

Leu Lys Lys Tyr Thr Leu Glu Asp Val Ser Arg His Asn Thr Pro Ala  
35 40 45

Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp  
50 55 60

Ile Pro Asn His Pro Gly Gly Ser Leu Ile His Val Lys Ala Gly Gln  
65 70 75 80

Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys  
85 90 95

Met Leu Ala Lys Tyr Cys Ile Gly Glu Leu Val Pro Ser Ala Gly Asp  
100 105 110

Asp Lys Phe Lys Lys Ala Thr Leu Glu Tyr Ala Asp Ala Glu Asn Glu  
115 120 125

Asp Phe Tyr Leu Val Val Lys Gln Arg Val Glu Ser Tyr Phe Lys Ser  
130 135 140



Asn Lys Ile Asn Pro Gln Ile His Pro His Met Ile Leu Lys Ser Leu  
 145 150 155 160

Phe Ile Leu Gly Gly Tyr Phe Ala Ser Tyr Tyr Leu Ala Phe Phe Trp  
 165 170 175

Ser Ser Ser Val Leu Val Ser Leu Phe Phe Ala Leu Trp Met Gly Phe  
 180 185 190

Phe Ala Ala Glu Val Gly Val Ser Ile Gln His Asp Gly Asn His Gly  
 195 200 205

Ser Tyr Thr Lys Trp Arg Gly Phe Gly Tyr Ile Met Gly Ala Ser Leu  
 210 215 220

Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Val  
 225 230 235 240

Gly His His Ser Phe Thr Asn Val Asp Asn Tyr Asp Pro Asp Ile Arg  
 245 250 255

Val Lys Asp Pro Asp Val Arg Arg Val Ala Thr Thr Gln Pro Arg Gln  
 260 265 270

Trp Tyr His Ala Tyr Gln His Ile Tyr Leu Ala Val Leu Tyr Gly Thr  
 275 280 285

Leu Ala Leu Lys Ser Ile Phe Leu Asp Asp Phe Leu Ala Tyr Phe Thr  
 290 295 300

Gly Ser Ile Gly Pro Val Lys Val Ala Lys Met Thr Pro Leu Glu Phe  
 305 310 315 320

Asn Ile Phe Phe Gln Gly Lys Leu Leu Tyr Ala Phe Tyr Met Phe Val  
 325 330 335

Leu Pro Ser Val Tyr Gly Val His Ser Gly Gly Thr Phe Leu Ala Leu  
 340 345 350

Tyr Val Ala Ser Gln Leu Ile Thr Gly Trp Met Leu Ala Phe Leu Phe  
 355 360 365

Gln Val Ala His Val Val Asp Asp Val Ala Phe Pro Thr Pro Glu Gly  
 370 375 380

Gly Lys Val Lys Gly Gly Trp Ala Ala Met Gln Val Ala Thr Thr Thr  
 385 390 395 400

Asp Phe Ser Pro Arg Ser Trp Phe Trp Gly His Val Ser Gly Gly Leu  
 405 410 415

Asn Asn Gln Ile Glu His His Leu Phe Pro Gly Val Cys His Val His  
 420 425 430

Tyr Pro Ala Ile Gln Pro Ile Val Glu Lys Thr Cys Lys Glu Phe Asp  
 435 440 445

Val Pro Tyr Val Ala Tyr Pro Thr Phe Trp Thr Ala Leu Arg Ala His  
 450 455 460

Phe Ala His Leu Lys Lys Val Gly Leu Thr Glu Phe Arg Leu Asp Gly  
 465 470 475 480

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 <213> Thraustrochytrium

<220>  
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 <222> (1)..(1320)  
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 gag gcg aac ggc gac aag cgg aaa acg att ctg atc gag ggc gtc ctg 96  
 Glu Ala Asn Gly Asp Lys Arg Lys Thr Ile Leu Ile Glu Gly Val Leu  
 20 25 30  
 tac gac gcg acg aac ttt aag cac ccg ggc ggt tcg atc atc aac ttc 144  
 Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe  
 35 40 45  
 ttg acc gag ggc gag gcc ggc gtg gac gcg acg cag gcg tac cgc gag 192  
 Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu  
 50 55 60  
 ttt cat cag cgg tcc ggc aag gcc gac aag tac ctc aag tcg ctg ccg 240  
 Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro  
 65 70 75 80  
 aag ctg gat gcg tcc aag gtg gag tcg cgg ttc tcg gcc aaa gag cag 288  
 Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln  
 85 90 95  
 gcg cgg cgc gac gcc atg acg cgc gac tac gcg gcc ttt cgc gag gag 336  
 Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu  
 100 105 110  
 ctc gtc gcc gag ggg tac ttt gac ccg tcg atc ccg cac atg att tac 384  
 Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr  
 115 120 125  
 cgc gtc gtg gag atc gtg gcg ctc ttc gcg ctc tcg ttc tgg ctc atg 432  
 Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met  
 130 135 140  
 tcc aag gcc tcg ccc acc tcg ctc gtg ctg ggc gtg gtg atg aac ggc 480  
 Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly

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tcg ttc acg ggc gtc atc tgg ctc gac gac cgg atg tgc gag ttc ttc Ser Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Met Cys Glu Phe Phe 180 185 190				576
tac ggc gtc ggc tgc ggc atg agc ggg cac tac tgg aag aac cag cac Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln His 195 200 205				624
agc aag cac cac gcc gcg ccc aac cgc ctc gag cac gat gtc gat ctc Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val Asp Leu 210 215 220				672
aac acg ctg ccc ctg gtc gcc ttt aac gag cgc gtc gtg cgc aag gtc Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val Arg Lys Val 225 230 235 240				720
aag ccg gga tcg ctg ctg gcg ctc tgg ctg cgc gtg cag gcg tac ctc Lys Pro Gly Ser Leu Leu Ala Leu Trp Leu Arg Val Gln Ala Tyr Leu 245 250 255				768
ttt gcg ccc gtc tcg tgc ctg ctc atc ggc ctt ggc tgg acg ctc tac Phe Ala Pro Val Ser Cys Leu Leu Ile Gly Leu Gly Trp Thr Leu Tyr 260 265 270				816
ctg cac ccg cgc tac atg ctg cgc acc aag cgg cac atg gag ttc gtc Leu His Pro Arg Tyr Met Leu Arg Thr Lys Arg His Met Glu Phe Val 275 280 285				864
tgg atc ttc gcg cgc tac att ggc tgg ttc tcg ctc atg ggc gct ctc Trp Ile Phe Ala Arg Tyr Ile Gly Trp Phe Ser Leu Met Gly Ala Leu 290 295 300				912
ggc tac tcg ccg ggc acc tcg gtc ggg atg tac ctg tgc tcg ttc ggc Gly Tyr Ser Pro Gly Thr Ser Val Gly Met Tyr Leu Cys Ser Phe Gly 305 310 315 320				960
ctc ggc tgc att tac att ttc ctg cag ttc gcc gtc agc cac acg cac Leu Gly Cys Ile Tyr Ile Phe Leu Gln Phe Ala Val Ser His Thr His 325 330 335				1008
ctg ccg gtg acc aac ccg gag gac cag ctg cac tgg ctc gag tac gcg Leu Pro Val Thr Asn Pro Glu Asp Gln Leu His Trp Leu Glu Tyr Ala 340 345 350				1056
gcc gac cac acg gtg aac att agc acc aag tcc tgg ctc gtc acg tgg Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp Leu Val Thr Trp 355 360 365				1104
tgg atg tcg aac ctg aac ttt cag atc gag cac cac ctc ttc ccc acg Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr 370 375 380				1152
gcg ccg cag ttc cgc ttc aag gaa atc agt cct cgc gtc gag gcc ctc Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu 385 390 395 400				1200
ttc aag cgc cac aac ctc ccg tac tac gac ctg ccc tac acg agc gcg Phe Lys Arg His Asn Leu Pro Tyr Tyr Asp Leu Pro Tyr Thr Ser Ala 405 410 415				1248
gtc tcg acc acc ttt gcc aat ctt tat tcc gtc ggc cac tcg gtc ggc Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly 420 425 430 435 440 445				1296

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 20                      25                      30  
  
 Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe  
 35                      40                      45  
  
 Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu  
 50                      55                      60  
  
 Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro  
 65                      70                      75                      80  
  
 Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln  
 85                      90                      95  
  
 Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu  
 100                      105                      110  
  
 Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr  
 115                      120                      125  
  
 Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met  
 130                      135                      140  
  
 Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly  
 145                      150                      155                      160  
  
 Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly  
 165                      170                      175  
  
 Ser Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Met Cys Glu Phe Phe  
 180                      185                      190  
  
 Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln His  
 195                      200                      205  
  
 Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val Asp Leu  
 210                      215                      220

Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val Arg Lys Val  
 225 230 235 240

Lys Pro Gly Ser Leu Leu Ala Leu Trp Leu Arg Val Gln Ala Tyr Leu  
 245 250 255

Phe Ala Pro Val Ser Cys Leu Leu Ile Gly Leu Gly Trp Thr Leu Tyr  
 260 265 270

Leu His Pro Arg Tyr Met Leu Arg Thr Lys Arg His Met Glu Phe Val  
 275 280 285

Trp Ile Phe Ala Arg Tyr Ile Gly Trp Phe Ser Leu Met Gly Ala Leu  
 290 295 300

Gly Tyr Ser Pro Gly Thr Ser Val Gly Met Tyr Leu Cys Ser Phe Gly  
 305 310 315 320

Leu Gly Cys Ile Tyr Ile Phe Leu Gln Phe Ala Val Ser His Thr His  
 325 330 335

Leu Pro Val Thr Asn Pro Glu Asp Gln Leu His Trp Leu Glu Tyr Ala  
 340 345 350

Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp Leu Val Thr Trp  
 355 360 365

Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr  
 370 375 380

Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu  
 385 390 395 400

Phe Lys Arg His Asn Leu Pro Tyr Tyr Asp Leu Pro Tyr Thr Ser Ala  
 405 410 415

Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly  
 420 425 430

Ala Asp Thr Lys Lys Gln Asp  
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 <213> Mortierella alpina  
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cat aac acc aag gac gac cta ctc ttg gcc atc cgc ggc agg gtg tac	96
His Asn Thr Lys Asp Asp Leu Leu Leu Ala Ile Arg Gly Arg Val Tyr	
20 25 30	
gat gtc aca aag ttc ttg agc cgc cat cct ggt gga gtg gac act ctc	144
Asp Val Thr Lys Phe Leu Ser Arg His Pro Gly Gly Val Asp Thr Leu	
35 40 45	
ctg ctc gga gct ggc cga gat gtt act ccg gtc ttt gag atg tat cac	192
Leu Leu Gly Ala Gly Arg Asp Val Thr Pro Val Phe Glu Met Tyr His	
50 55 60	
gcg ttt ggg gct gca gat gcc att atg aag aag tac tat gtc ggt aca	240
Ala Phe Gly Ala Ala Asp Ala Ile Met Lys Lys Tyr Tyr Val Gly Thr	
65 70 75 80	
ctg gtc tcg aat gag ctg ccc atc ttc ccg gag cca acg gtg ttc cac	288
Leu Val Ser Asn Glu Leu Pro Ile Phe Pro Glu Pro Thr Val Phe His	
85 90 95	
aaa acc atc aag acg aga gtc gag ggc tac ttt acg gat cgg aac att	336
Lys Thr Ile Lys Thr Arg Val Glu Gly Tyr Phe Thr Asp Arg Asn Ile	
100 105 110	
gat ccc aag aat aga cca gag atc tgg gga cga tac gct ctt atc ttt	384
Asp Pro Lys Asn Arg Pro Glu Ile Trp Gly Arg Tyr Ala Leu Ile Phe	
115 120 125	
gga tcc ttg atc gct tcc tac tac gcg cag ctc ttt gtg cct ttc gtt	432
Gly Ser Leu Ile Ala Ser Tyr Tyr Ala Gln Leu Phe Val Pro Phe Val	
130 135 140	
gtc gaa cgc aca tgg ctt cag gtg gtg ttt gca atc atc atg gga ttt	480
Val Glu Arg Thr Trp Leu Gln Val Val Phe Ala Ile Ile Met Gly Phe	
145 150 155 160	
gcg tgc gca caa gtc gga ctc aac cct ctt cat gat gcg tct cac ttt	528
Ala Cys Ala Gln Val Gly Leu Asn Pro Leu His Asp Ala Ser His Phe	
165 170 175	
tca gtg acc cac aac ccc act gtc tgg aag att ctg gga gcc acg cac	576
Ser Val Thr His Asn Pro Thr Val Trp Lys Ile Leu Gly Ala Thr His	
180 185 190	
gac ttt ttc aac gga gca tcg tac ctg gtg tgg atg tac caa cat atg	624
Asp Phe Phe Asn Gly Ala Ser Tyr Leu Val Trp Met Tyr Gln His Met	
195 200 205	
ctc ggc cat cac ccc tac acc aac att gct gga gca gat ccc gac gtg	672
Leu Gly His His Pro Tyr Thr Asn Ile Ala Gly Ala Asp Pro Asp Val	
210 215 220	
tcg acg tct gag ccc gat gtt cgt cgt atc aag ccc aac caa aag tgg	720
Ser Thr Ser Glu Pro Asp Val Arg Arg Ile Lys Pro Asn Gln Lys Trp	
225 230 235 240	
ttt gtc aac cac atc aac cag cac atg ttt gtt cct ttc ctg tac gga	768
Phe Val Asn His Ile Asn Gln His Met Phe Val Pro Phe Leu Tyr Gly	
245 250 255	
ctg ctg gcg ttc aag gtg cgc att cag gac atc aac att ttg tac ttt	816
Leu Leu Ala Phe Lys Val Arg Ile Gln Asp Ile Asn Ile Leu Tyr Phe	

260	265	270	
gtc aag acc aat gac gct att cgt gtc aat ccc atc tcg aca tgg cac			864
Val Lys Thr Asn Asp Ala Ile Arg Val Asn Pro Ile Ser Thr Trp His			
275	280	285	
act gtg atg ttc tgg ggc ggc aag gct ttc ttt gtc tgg tat cgc ctg			912
Thr Val Met Phe Trp Gly Gly Lys Ala Phe Phe Val Trp Tyr Arg Leu			
290	295	300	
att gtt ccc ctg cag tat ctg ccc ctg ggc aag gtg ctg ctc ttg ttc			960
Ile Val Pro Leu Gln Tyr Leu Pro Leu Gly Lys Val Leu Leu Leu Phe			
305	310	315	320
acg gtc gcg gac atg gtg tcg tct tac tgg ctg gcg ctg acc ttc cag			1008
Thr Val Ala Asp Met Val Ser Ser Tyr Trp Leu Ala Leu Thr Phe Gln			
325	330	335	
gcg aac cac gtt gtt gag gaa gtt cag tgg ccg ttg cct gac gag aac			1056
Ala Asn His Val Val Glu Glu Val Gln Trp Pro Leu Pro Asp Glu Asn			
340	345	350	
ggg atc atc caa aag gac tgg gca gct atg cag gtc gag act acg cag			1104
Gly Ile Ile Gln Lys Asp Trp Ala Ala Met Gln Val Glu Thr Thr Gln			
355	360	365	
gat tac gca cac gat tcg cac ctc tgg acc agc atc act ggc agc ttg			1152
Asp Tyr Ala His Asp Ser His Leu Trp Thr Ser Ile Thr Gly Ser Leu			
370	375	380	
aac tac cag gct gtg cac cat ctg ttc ccc aac gtg tcg cag cac cat			1200
Asn Tyr Gln Ala Val His His Leu Phe Pro Asn Val Ser Gln His His			
385	390	395	400
tat ccc gat att ctg gcc atc atc aag aac acc tgc agc gag tac aag			1248
Tyr Pro Asp Ile Leu Ala Ile Ile Lys Asn Thr Cys Ser Glu Tyr Lys			
405	410	415	
gtt cca tac ctt gtc aag gat acg ttt tgg caa gca ttt gct tca cat			1296
Val Pro Tyr Leu Val Lys Asp Thr Phe Trp Gln Ala Phe Ala Ser His			
420	425	430	
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1	5	10	15
His Asn Thr Lys Asp Asp Leu Leu Leu Ala Ile Arg Gly Arg Val Tyr			
20	25	30	
Asp Val Thr Lys Phe Leu Ser Arg His Pro Gly Gly Val Asp Thr Leu			
35	40	45	
Leu Leu Gly Ala Gly Arg Asp Val Thr Pro Val Phe Glu Met Tyr His			
50	55	60	

Ala Phe Gly Ala Ala Asp Ala Ile Met Lys Lys Tyr Tyr Val Gly Thr  
65 70 75 80

Leu Val Ser Asn Glu Leu Pro Ile Phe Pro Glu Pro Thr Val Phe His  
85 90 95

Lys Thr Ile Lys Thr Arg Val Glu Gly Tyr Phe Thr Asp Arg Asn Ile  
100 105 110

Asp Pro Lys Asn Arg Pro Glu Ile Trp Gly Arg Tyr Ala Leu Ile Phe  
115 120 125

Gly Ser Leu Ile Ala Ser Tyr Tyr Ala Gln Leu Phe Val Pro Phe Val  
130 135 140

Val Glu Arg Thr Trp Leu Gln Val Val Phe Ala Ile Ile Met Gly Phe  
145 150 155 160

Ala Cys Ala Gln Val Gly Leu Asn Pro Leu His Asp Ala Ser His Phe  
165 170 175

Ser Val Thr His Asn Pro Thr Val Trp Lys Ile Leu Gly Ala Thr His  
180 185 190

Asp Phe Phe Asn Gly Ala Ser Tyr Leu Val Trp Met Tyr Gln His Met  
195 200 205

Leu Gly His His Pro Tyr Thr Asn Ile Ala Gly Ala Asp Pro Asp Val  
210 215 220

Ser Thr Ser Glu Pro Asp Val Arg Arg Ile Lys Pro Asn Gln Lys Trp  
225 230 235 240

Phe Val Asn His Ile Asn Gln His Met Phe Val Pro Phe Leu Tyr Gly  
245 250 255

Leu Leu Ala Phe Lys Val Arg Ile Gln Asp Ile Asn Ile Leu Tyr Phe  
260 265 270

Val Lys Thr Asn Asp Ala Ile Arg Val Asn Pro Ile Ser Thr Trp His  
275 280 285

Thr Val Met Phe Trp Gly Gly Lys Ala Phe Phe Val Trp Tyr Arg Leu  
290 295 300

Ile Val Pro Leu Gln Tyr Leu Pro Leu Gly Lys Val Leu Leu Leu Phe  
305 310 315 320

Thr Val Ala Asp Met Val Ser Ser Tyr Trp Leu Ala Leu Thr Phe Gln  
325 330 335



Ala Asn His Val Val Glu Glu Val Gln Trp Pro Leu Pro Asp Glu Asn  
 340 345 350

Gly Ile Ile Gln Lys Asp Trp Ala Ala Met Gln Val Glu Thr Thr Gln  
 355 360 365

Asp Tyr Ala His Asp Ser His Leu Trp Thr Ser Ile Thr Gly Ser Leu  
 370 375 380

Asn Tyr Gln Ala Val His His Leu Phe Pro Asn Val Ser Gln His His  
 385 390 395 400

Tyr Pro Asp Ile Leu Ala Ile Ile Lys Asn Thr Cys Ser Glu Tyr Lys  
 405 410 415

Val Pro Tyr Leu Val Lys Asp Thr Phe Trp Gln Ala Phe Ala Ser His  
 420 425 430

Leu Glu His Leu Arg Val Leu Gly Leu Arg Pro Lys Glu Glu  
 435 440 445

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 <213> Caenorhabditis elegans

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 gga aaa tgg tgt caa att gac gat gct gtc ctg aga tca cat cca ggt 96  
 Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly  
 20 25 30  
 ggt agt gca att act acc tat aaa aat atg gat gcc act acc gta ttc 144  
 Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe  
 35 40 45  
 cac aca ttc cat act ggt tct aaa gaa gcg tat caa tgg ctg aca gaa 192  
 His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu  
 50 55 60  
 ttg aaa aaa gag tgc cct aca caa gaa cca gag atc cca gat att aag 240  
 Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys  
 65 70 75 80  
 gat gac cca atc aaa gga att gat gat gtg aac atg gga act ttc aat 288  
 Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn  
 85 90 95  
 att tct gag aaa cga tct gcc caa ata aat aaa agt ttc act gat cta 336  
 Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu

100	105	110	
cgt atg cga gtt cgt gca gaa gga ctt atg gat gga tct cct ttg ttc Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe 115 120 125			384
tac att aga aaa att ctt gaa aca atc ttc aca att ctt ttt gca ttc Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe 130 135 140			432
tac ctt caa tac cac aca tat tat ctt cca tca gct att cta atg gga Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly 145 150 155 160			480
gtt gcg tgg caa caa ttg gga tgg tta atc cat gaa ttc gca cat cat Val Ala Trp Gln Glu Leu Gly Trp Leu Ile His Glu Phe Ala His His 165 170 175			528
cag ttg ttc aaa aac aga tac tac aat gat ttg gcc agc tat ttc gtt Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val 180 185 190			576
gga aac ttt tta caa gga ttc tca tct ggt ggt tgg aaa gag cag cac Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His 195 200 205			624
aat gtg cat cac gca gcc aca aat gtt gtt gga cga gac gga gat ctt Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu 210 215 220			672
gat tta gtc cca ttc tat gct aca gtg gca gaa cat ctc aac aat tat Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr 225 230 235 240			720
tct cag gat tca tgg gtt atg act cta ttc aga tgg caa cat gtt cat Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His 245 250 255			768
tgg aca ttc atg tta cca ttc ctc cgt ctc tcg tgg ctt ctt cag tca Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser 260 265 270			816
atc att ttt gtt agt cag atg cca act cat tat tat gac tat tac aga Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg 275 280 285			864
aat act gcg att tat gaa cag gtt ggt ctc tct ttg cac tgg gct tgg Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp 290 295 300			912
tca ttg ggt caa ttg tat ttc cta ccc gat tgg tca act aga ata atg Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met 305 310 315 320			960
ttc ttc ctt gtt tct cat ctt gtt gga ggt ttc ctg ctc tct cat gta Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val 325 330 335			1008
gtt act ttc aat cat tat tca gtg gag aag ttt gca ttg agc tcg aac Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn 340 345 350			1056
atc atg tca aat tac gct tgt ctt caa atc atg acc aca aga aat atg Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met 355 360 365			1104
aga cct gga aga ttc att gac tgg ctt tgg gga ggt ctt aac tat cag Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln			1152

27

370                      375                      380  
 att gag cac cat ctt ttc cca acg atg cca cga cac aac ttg aac act 1200  
 ile glu his his leu phe pro thr met pro arg his asn leu asn thr  
 385                      390                      395                      400  
 gtt atg cca ctt gtt aag gag ttt gca gca gca aat ggt tta cca tac 1248  
 val met pro leu val lys glu phe ala ala ala asn gly leu pro tyr  
 405                      410                      415  
 atg gtc gac gat tat ttc aca gga ttc tgg ctt gaa att gag caa ttc 1296  
 met val asp asp tyr phe thr gly phe trp leu glu ile glu gln phe  
 420                      425                      430  
 cga aat att gca aat gtt gct gct aaa ttg act aaa aag att gcc tag 1344  
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 Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly  
 20                      25                      30  
 Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe  
 35                      40                      45  
 His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu  
 50                      55                      60  
 Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys  
 65                      70                      75                      80  
 Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn  
 85                      90                      95  
 Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu  
 100                      105                      110  
 Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe  
 115                      120                      125  
 Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe  
 130                      135                      140  
 Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly  
 145                      150                      155                      160  
 Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His  
 165                      170                      175

Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val  
 180 185 190

Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His  
 195 200 205

Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu  
 210 215 220

Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr  
 225 230 235 240

Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His  
 245 250 255

Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser  
 260 265 270

Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg  
 275 280 285

Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp  
 290 295 300

Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met  
 305 310 315 320

Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val  
 325 330 335

Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn  
 340 345 350

Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met  
 355 360 365

Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln  
 370 375 380

Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr  
 385 390 395 400

Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr  
 405 410 415

Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe  
 420 425 430

Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala  
 435 440 445



200	205	210	
tat ata cca ttc ctt gtt gtg tct tcc aag ttt ttt ggt tca ctc acc Tyr Ile Pro Phe Leu Val Val Ser Ser Lys Phe Phe Gly Ser Leu Thr 215 220 225			728
tct cat ttc tat gag aaa agg ttg act ttt gac tct tta tca aga ttc Ser His Phe Tyr Glu Lys Arg Leu Thr Phe Asp Ser Leu Ser Arg Phe 230 235 240 245			776
ttt gta agt tat caa cat tgg aca ttt tac cct att atg tgt gct gct Phe Val Ser Tyr Gln His Trp Thr Phe Tyr Pro Ile Met Cys Ala Ala 250 255 260			824
agg ctc aat atg tat gta caa tct ctc ata atg ttg ttg acc aag aga Arg Leu Asn Met Tyr Val Gln Ser Leu Ile Met Leu Leu Thr Lys Arg 265 270 275			872
aat gtg tcc tat cga gct cag gaa ctc ttg gga tgc cta gtg ttc tcg Asn Val Ser Tyr Arg Ala Gln Glu Leu Leu Gly Cys Leu Val Phe Ser 280 285 290			920
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att atg ttt gtt att gca agt tta tca gtg act gga atg caa caa gtt Ile Met Phe Val Ile Ala Ser Leu Ser Val Thr Gly Met Gln Gln Val 310 315 320 325			1016
cag ttc tcc ttg aac cac ttc tct tca agt gtt tat gtt gga aag cct Gln Phe Ser Leu Asn His Phe Ser Ser Ser Val Tyr Val Gly Lys Pro 330 335 340			1064
aaa ggg aat aat tgg ttt gag aaa caa acg gat ggg aca ctt gac att Lys Gly Asn Asn Trp Phe Glu Lys Gln Thr Asp Gly Thr Leu Asp Ile 345 350 355			1112
tct tgt cct cct tgg atg gat tgg ttt cat ggt gga ttg caa ttc caa Ser Cys Pro Pro Trp Met Asp Trp Phe His Gly Gly Leu Gln Phe Gln 360 365 370			1160
att gag cat cat ttg ttt ccc aag atg cct aga tgc aac ctt agg aaa Ile Glu His His Leu Phe Pro Lys Met Pro Arg Cys Asn Leu Arg Lys 375 380 385			1208
atc tcg ccc tac gtg atc gag tta tgc aag aaa cat aat ttg cct tac Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys His Asn Leu Pro Tyr 390 395 400 405			1256
aat tat gca tct ttc tcc aag gcc aat gaa atg aca ctc aga aca ttg Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met Thr Leu Arg Thr Leu 410 415 420			1304
agg aac aca gca ttg cag gct agg gat ata acc aag ccg ctc ccg aag Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr Lys Pro Leu Pro Lys 425 430 435			1352
aat ttg gta tgg gaa gct ctt cac act cat ggt taa aattaccctt Asn Leu Val Trp Glu Ala Leu His Thr His Gly 440 445			1398
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gaggttttgc tttcatctcc attattgatg aataaggagt tgcattattgt caattgttgt			1578

gctcaatatc tgatattttg gaatgtactt tgtaccactg tgttttcagt tgaagtcac 1638  
 gtgtacttct atagactttg tttaaatggt tatgtcatgt tattt 1683

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 <212> PRT  
 <213> Borago officinalis

<400> 18

Met Ala Ala Gln Ile Lys Lys Tyr Ile Thr Ser Asp Glu Leu Lys Asn  
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His Asp Lys Pro Gly Asp Leu Trp Ile Ser Ile Gln Gly Lys Ala Tyr  
 20 25 30

Asp Val Ser Asp Trp Val Lys Asp His Pro Gly Gly Ser Phe Pro Leu  
 35 40 45

Lys Ser Leu Ala Gly Gln Glu Val Thr Asp Ala Phe Val Ala Phe His  
 50 55 60

Pro Ala Ser Thr Trp Lys Asn Leu Asp Lys Phe Phe Thr Gly Tyr Tyr  
 65 70 75 80

Leu Lys Asp Tyr Ser Val Ser Glu Val Ser Lys Asp Tyr Arg Lys Leu  
 85 90 95

Val Phe Glu Phe Ser Lys Met Gly Leu Tyr Asp Lys Lys Gly His Ile  
 100 105 110

Met Phe Ala Thr Leu Cys Phe Ile Ala Met Leu Phe Ala Met Ser Val  
 115 120 125

Tyr Gly Val Leu Phe Cys Glu Gly Val Leu Val His Leu Phe Ser Gly  
 130 135 140

Cys Leu Met Gly Phe Leu Trp Ile Gln Ser Gly Trp Ile Gly His Asp  
 145 150 155 160

Ala Gly His Tyr Met Val Val Ser Asp Ser Arg Leu Asn Lys Phe Met  
 165 170 175

Gly Ile Phe Ala Ala Asn Cys Leu Ser Gly Ile Ser Ile Gly Trp Trp  
 180 185 190

Lys Trp Asn His Asn Ala His His Ile Ala Cys Asn Ser Leu Glu Tyr  
 195 200 205

Asp Pro Asp Leu Gln Tyr Ile Pro Phe Leu Val Val Ser Ser Lys Phe  
 210 215 220

## 32

Phe Gly Ser Leu Thr Ser His Phe Tyr Glu Lys Arg Leu Thr Phe Asp  
 225 230 235 240

Ser Leu Ser Arg Phe Phe Val Ser Tyr Gln His Trp Thr Phe Tyr Pro  
 245 250 255

Ile Met Cys Ala Ala Arg Leu Asn Met Tyr Val Gln Ser Leu Ile Met  
 260 265 270

Leu Leu Thr Lys Arg Asn Val Ser Tyr Arg Ala Gln Glu Leu Leu Gly  
 275 280 285

Cys Leu Val Phe Ser Ile Trp Tyr Pro Leu Leu Val Ser Cys Leu Pro  
 290 295 300

Asn Trp Gly Glu Arg Ile Met Phe Val Ile Ala Ser Leu Ser Val Thr  
 305 310 315 320

Gly Met Gln Gln Val Gln Phe Ser Leu Asn His Phe Ser Ser Ser Val  
 325 330 335

Tyr Val Gly Lys Pro Lys Gly Asn Asn Trp Phe Glu Lys Gln Thr Asp  
 340 345 350

Gly Thr Leu Asp Ile Ser Cys Pro Pro Trp Met Asp Trp Phe His Gly  
 355 360 365

Gly Leu Gln Phe Gln Ile Glu His His Leu Phe Pro Lys Met Pro Arg  
 370 375 380

Cys Asn Leu Arg Lys Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys  
 385 390 395 400

His Asn Leu Pro Tyr Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met  
 405 410 415

Thr Leu Arg Thr Leu Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr  
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Lys Pro Leu Pro Lys Asn Leu Val Trp Glu Ala Leu His Thr His Gly  
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<400> 19



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att gac gtt gag cac ttg gca acg atg ccc ctc gtc agt gac ttc cta	96
Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu	
20 25 30	
aat gtc ctg gga acg act ttg ggc cag tgg agt ctt tcc act aca ttc	144
Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe	
35 40 45	
gct ttc aag agg ctc acg act aag aaa cac agt tcg gac atc tcg gtg	192
Ala Phe Lys Arg Leu Thr Thr Lys Lys His Ser Ser Asp Ile Ser Val	
50 55 60	
gag gca caa aaa gaa tcg gtt gcg cgg ggg cca gtt gag aat att tct	240
Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser	
65 70 75 80	
caa tcg gtt gcg cag ccc atc agg cgg agg tgg gtg cag gat aaa aag	288
Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys	
85 90 95	
ccg gtt act tac agc ctg aag gat gta gct tcg cac gat atg ccc cag	336
Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln	
100 105 110	
gac tgc tgg att ata atc aaa gag aag gtg tat gat gtg agc acc ttc	384
Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe	
115 120 125	
gct gag cag cac cct gga ggc acg gtt atc aac acc tac ttc gga cga	432
Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg	
130 135 140	
gac gcc aca gat gtt ttc tct act ttc cac gca tcc acc tca tgg aag	480
Asp Ala Thr Asp Val Phe Ser Thr Phe His Ala Ser Thr Ser Trp Lys	
145 150 155 160	
att ctt cag aat ttc tac atc ggg aac ctt gtt agg gag gag ccg act	528
Ile Leu Gln Asn Phe Tyr Ile Gly Asn Leu Val Arg Glu Glu Pro Thr	
165 170 175	
ttg gag ctg ctg aag gag tac aga gag ttg aga gcc ctt ttc ttg aga	576
Leu Glu Leu Leu Lys Glu Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg	
180 185 190	
gaa cag ctt ttc aag agt tcc aaa tcc tac tac ctt ttc aag act ctc	624
Glu Gln Leu Phe Lys Ser Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu	
195 200 205	
ata aat gtt tcc att gtt gcc aca agc att gcg ata atc agt ctg tac	672
Ile Asn Val Ser Ile Val Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr	
210 215 220	
aag tct tac cgg gcg gtt ctg tta tca gcc agt ttg atg ggc ttg ttt	720
Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe	
225 230 235 240	
att caa cag tgc gga tgg ttg tct cac gat ttt cta cac cat cag gta	768
Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val	
245 250 255	
ttt gag aca cgc tgg ctc aat gac gtt gtt ggc tat gtg gtc ggc aac	816
Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn	
260 265 270	

## 34

gtt gtt ctg gga ttc agt gtc tcg tgg tgg aag acc aag cac aac ctg Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu 275 280 285	864
cat cat gct gct ccg aat gaa tgc gac caa aag tac aca ccg att gat His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp 290 295 300	912
gag gat att gat act ctc ccc atc att gct tgg agt aaa gat ctc ttg Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu 305 310 315 320	960
gcc act gtt gag agc aag acc atg ttg cga gtt ctt cag tac cag cac Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His 325 330 335	1008
cta ttc ttt ttg gtt ctt ttg acg ttt gcc cgg gcg agt tgg cta ttt Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe 340 345 350	1056
tgg agc gcg gcc ttc act ctc agg ccc gag ttg acc ctt ggc gag aag Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys 355 360 365	1104
ctt ttg gag agg gga acg atg gct ttg cac tac att tgg ttt aat agt Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser 370 375 380	1152
gtt gcg ttt tat ctg ctc ccc gga tgg aaa cca gtt gta tgg atg gtg Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val 385 390 395 400	1200
gtc agc gag ctc atg tct ggt ttc ctg ctg gga tac gta ttt gta ctc Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu 405 410 415	1248
agt cac aat gga atg gag gtg tac aat acg tca aag gac ttc gtg aat Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn 420 425 430	1296
gcc cag att gca tcg act cgc gac atc aaa gca ggg gtg ttt aat gat Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp 435 440 445	1344
tgg ttc acc gga ggt ctc aac aga cag att gag cat cat cta ttt cca Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro 450 455 460	1392
acg atg ccc agg cac aac ctt aat aaa att tct cct cac gtg gag act Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr 465 470 475 480	1440
ttg tgc aag aag cat gga ctg gtc tac gaa gac gtg agc atg gct tcg Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser 485 490 495	1488
ggc act tac ccg gtt ttg aaa aca ctt aag gac gtt gcc gat gct gct Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala 500 505 510	1536
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 <211> 520  
 <212> PRT

&lt;213&gt; Ceratodon purpureus

&lt;400&gt; 20

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 1 5 10 15

Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu  
 20 25 30

Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe  
 35 40 45

Ala Phe Lys Arg Leu Thr Thr Lys Lys His Ser Ser Asp Ile Ser Val  
 50 55 60

Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser  
 65 70 75 80

Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys  
 85 90 95

Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln  
 100 105 110

Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe  
 115 120 125

Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg  
 130 135 140

Asp Ala Thr Asp Val Phe Ser Thr Phe His Ala Ser Thr Ser Trp Lys  
 145 150 155 160

Ile Leu Gln Asn Phe Tyr Ile Gly Asn Leu Val Arg Glu Glu Pro Thr  
 165 170 175

Leu Glu Leu Leu Lys Glu Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg  
 180 185 190

Glu Gln Leu Phe Lys Ser Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu  
 195 200 205

Ile Asn Val Ser Ile Val Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr  
 210 215 220

Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe  
 225 230 235 240

Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val  
 245 250 255

36

Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn  
260 265 270

Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu  
275 280 285

His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp  
290 295 300

Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu  
305 310 315 320

Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His  
325 330 335

Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe  
340 345 350

Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys  
355 360 365

Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser  
370 375 380

Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val  
385 390 395 400

Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu  
405 410 415

Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn  
420 425 430

Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp  
435 440 445

Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro  
450 455 460

Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr  
465 470 475 480

Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser  
485 490 495

Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala  
500 505 510

Ser His Gln Gln Leu Ala Ala Ser  
515 520

<210> 21  
 <211> 1434  
 <212> DNA  
 <213> *Phaeodactylum tricornutum*

<220>  
 <221> CDS  
 <222> (1)..(1434)  
 <223> Delta-6-Desaturase

<400> 21  
 atg ggc aaa gga ggg gac gct cgg gcc tcg aag ggc tca acg gcg gct 48  
 Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala  
 1 5 10 15  
 cgc aag atc agt tgg cag gaa gtc aag acc cac gcg tct ccg gag gac 96  
 Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp  
 20 25 30  
 gcc tgg atc att cac tcc aat aag gtc tac gac gtg tcc aac tgg cac 144  
 Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His  
 35 40 45  
 gaa cat ccc gga ggc gcc gtc att ttc acg cac gcc ggt gac gac atg 192  
 Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met  
 50 55 60  
 acg gac att ttc gct gcc ttt cac gca ccc gga tcg cag tcg ctc atg 240  
 Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met  
 65 70 75 80  
 aag aag ttc tac att ggc gaa ttg ctc ccg gaa acc acc ggc aag gag 288  
 Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu  
 85 90 95  
 ccg cag caa atc gcc ttt gaa aag ggc tac cgc gat ctg cgc tcc aaa 336  
 Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys  
 100 105 110  
 ctc atc atg atg ggc atg ttc aag tcc aac aag tgg ttc tac gtc tac 384  
 Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr  
 115 120 125  
 aag tgc ctc agc aac atg gcc att tgg gcc gcc gcc tgt gct ctc gtc 432  
 Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val  
 130 135 140  
 ttt tac tcg gac cgc ttc tgg gta cac ctg gcc agc gcc gtc atg ctg 480  
 Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu  
 145 150 155 160  
 gga aca ttc ttt cag cag tcg gga tgg ttg gca cac gac ttt ctg cac 528  
 Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His  
 165 170 175  
 cac cag gtc ttc acc aag cgc aag cac ggg gat ctc gga gga ctc ttt 576  
 His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly Leu Phe  
 180 185 190  
 tgg ggg aac ctc atg cag ggt tac tcc gta cag tgg tgg aaa aac aag 624  
 Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys  
 195 200 205  
 cac aac gga cac cac gcc gtc ccc aac ctc cac tgc tcc tcc gca gtc 672  
 His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val  
 210 215 220

38

gcg caa gat ggg gac ccg gac atc gat acc atg ccc ctt ctc gcc tgg 720  
 Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp  
 225 230 235 240

tcc gtc cag caa gcc cag tct tac cgg gaa ctc caa gcc gac gga aag 768  
 Ser Val Gln Gln Ala Gln Ser Tyr Arg Glu Leu Gln Ala Asp Gly Lys  
 245 250 255

gat tcg ggt ttg gtc aag ttc atg atc cgt aac caa tcc tac ttt tac 816  
 Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser Tyr Phe Tyr  
 260 265 270

ttt ccc atc ttg ttg ctc gcc cgc ctg tcg tgg ttg aac gag tcc ttc 864  
 Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe  
 275 280 285

aag tgc gcc ttt ggg ctt gga gct gcg tcg gag aac gct gct ctc gaa 912  
 Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala Ala Leu Glu  
 290 295 300

ctc aag gcc aag ggt ctt cag tac ccc ctt ttg gaa aag gct ggc atc 960  
 Leu Lys Ala Lys Gly Leu Gln Tyr Pro Leu Leu Glu Lys Ala Gly Ile  
 305 310 315 320

ctg ctg cac tac gct tgg atg ctt aca gtt tcg tcc ggc ttt gga cgc 1008  
 Leu Leu His Tyr Ala Trp Met Leu Thr Val Ser Ser Gly Phe Gly Arg  
 325 330 335

ttc tcg ttc gcg tac acc gca ttt tac ttt cta acc gcg acc gcg tcc 1056  
 Phe Ser Phe Ala Tyr Thr Ala Phe Tyr Phe Leu Thr Ala Thr Ala Ser  
 340 345 350

tgt gga ttc ttg ctc gcc att gtc ttt ggc ctc ggc cac aac ggc atg 1104  
 Cys Gly Phe Leu Leu Ala Ile Val Phe Gly Leu Gly His Asn Gly Met  
 355 360 365

gcc acc tac aat gcc gac gcc cgt ccg gac ttc tgg aag ctc caa gtc 1152  
 Ala Thr Tyr Asn Ala Asp Ala Arg Pro Asp Phe Trp Lys Leu Gln Val  
 370 375 380

acc acg act cgc aac gtc acg ggc gga cac ggt ttc ccc caa gcc ttt 1200  
 Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe  
 385 390 395 400

gtc gac tgg ttc tgt ggt ggc ctc cag tac caa gtc gac cac cac tta 1248  
 Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu  
 405 410 415

ttc ccc agc ctg ccc cga cac aat ctg gcc aag aca cac gca ctg gtc 1296  
 Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val  
 420 425 430

gaa tcg ttc tgc aag gag tgg ggt gtc cag tac cac gaa gcc gac ctt 1344  
 Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu  
 435 440 445

gtg gac ggg acc atg gaa gtc ttg cac cat ttg ggc agc gtg gcc ggc 1392  
 Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly  
 450 455 460

gaa ttc gtc gtg gat ttt gta cgc gat gga ccc gcc atg taa 1434  
 Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met  
 465 470 475

<210> 22  
 <211> 477  
 <212> PRT

&lt;213&gt; Phaeodactylum tricornutum

&lt;400&gt; 22

Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala  
 1 5 10 15

Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp  
 20 25 30

Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His  
 35 40 45

Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met  
 50 55 60

Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met  
 65 70 75 80

Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu  
 85 90 95

Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys  
 100 105 110

Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr  
 115 120 125

Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val  
 130 135 140

Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu  
 145 150 155 160

Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His  
 165 170 175

His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly Leu Phe  
 180 185 190

Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys  
 195 200 205

His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val  
 210 215 220

Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp  
 225 230 235 240

Ser Val Gln Gln Ala Gln Ser Tyr Arg Glu Leu Gln Ala Asp Gly Lys  
 245 250 255

40

Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser Tyr Phe Tyr  
 260 265 270

Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe  
 275 280 285

Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala Ala Leu Glu  
 290 295 300

Leu Lys Ala Lys Gly Leu Gln Tyr Pro Leu Leu Glu Lys Ala Gly Ile  
 305 310 315 320

Leu Leu His Tyr Ala Trp Met Leu Thr Val Ser Ser Gly Phe Gly Arg  
 325 330 335

Phe Ser Phe Ala Tyr Thr Ala Phe Tyr Phe Leu Thr Ala Thr Ala Ser  
 340 345 350

Cys Gly Phe Leu Leu Ala Ile Val Phe Gly Leu Gly His Asn Gly Met  
 355 360 365

Ala Thr Tyr Asn Ala Asp Ala Arg Pro Asp Phe Trp Lys Leu Gln Val  
 370 375 380

Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe  
 385 390 395 400

Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu  
 405 410 415

Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val  
 420 425 430

Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu  
 435 440 445

Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly  
 450 455 460

Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met  
 465 470 475

<210> 23  
 <211> 1578  
 <212> DNA  
 <213> *Physcomitrella patens*

<220>  
 <221> CDS  
 <222> (1)..(1578)  
 <223> Delta-6-Desaturase

<400> 23



atg gta ttc gcg ggc ggt gga ctt cag cag ggc tct ctc gaa gaa aac	48
Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn	
1 5 10 15	
atc gac gtc gag cac att gcc agt atg tct ctc ttc agc gac ttc ttc	96
Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe	
20 25 30	
agt tat gtg tct tca act gtt ggt tgc tgg agc gta cac agt ata caa	144
Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln	
35 40 45	
cct ttg aag cgc ctg acg agt aag aag cgt gtt tgc gaa agc gct gcc	192
Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala	
50 55 60	
gtg caa tgt ata tca gct gaa gtt cag aga aat tgc agt acc cag gga	240
Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly	
65 70 75 80	
act gcg gag gca ctc gca gaa tca gtc gtg aag ccc acg aga cga agg	288
Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg	
85 90 95	
tca tct cag tgg aag aag tgc aca cac ccc cta tca gaa gta gca gta	336
Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val	
100 105 110	
cac aac aag cca agc gat tgc tgg att gtt gta aaa aac aag gtg tat	384
His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr	
115 120 125	
gat gtt tcc aat ttt gcg gac gag cat ccc gga gga tca gtt att agt	432
Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser	
130 135 140	
act tat ttt gga cga gac ggc aca gat gtt ttc tct agt ttt cat gca	480
Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala	
145 150 155 160	
gct tct aca tgg aaa att ctt caa gac ttt tac att ggt gac gtg gag	528
Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu	
165 170 175	
agg gtg gag ccg act cca gag ctg ctg aaa gat ttc cga gaa atg aga	576
Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg	
180 185 190	
gct ctt ttc ctg agg gag caa ctt ttc aaa agt tgc aaa ttg tac tat	624
Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr	
195 200 205	
gtt atg aag ctg ctc acg aat gtt gct att ttt gct gcg agc att gca	672
Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala	
210 215 220	
ata ata tgt tgg agc aag act att tca gcg gtt ttg gct tca gct tgt	720
Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys	
225 230 235 240	
atg atg gct ctg tgt ttc caa cag tgc gga tgg cta tcc cat gat ttt	768
Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe	
245 250 255	
ctc cac aat cag gtg ttt gag aca cgc tgg ctt aat gaa gtt gtc ggg	816
Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly	
260 265 270	

42

tat gtg atc ggc aac gcc gtt ctg ggg ttt agt aca ggg tgg tgg aag Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys 275 280 285	864
gag aag cat aac ctt cat cat gct gct cca aat gaa tgc gat cag act Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr 290 295 300	912
tac caa cca att gat gaa gat att gat act ctc ccc ctc att gcc tgg Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp 305 310 315 320	960
agc aag gac ata ctg gcc aca gtt gag aat aag aca ttc ttg cga atc Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile 325 330 335	1008
ctc caa tac cag cat ctg ttc ttc atg ggt ctg tta ttt ttc gcc cgt Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg 340 345 350	1056
ggg agt tgg ctc ttt tgg agc tgg aga tat acc tct aca gca gtg ctc Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu 355 360 365	1104
tca cct gtc gac agg ttg ttg gag aag gga act gtt ctg ttt cac tac Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr 370 375 380	1152
ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc cct ggt tgg aag cca Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro 385 390 395 400	1200
tta gta tgg atg gcg gtg act gag ctc atg tcc ggc atg ctg ctg ggc Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly 405 410 415	1248
ttt gta ttt gta ctt agc cac aat ggg atg gag gtt tat aat tgc tct Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser 420 425 430	1296
aaa gaa ttc gtg agt gca cag atc gta tcc aca cgg gat atc aaa gga Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly 435 440 445	1344
aac ata ttc aac gac tgg ttc act ggt ggc ctt aac agg caa ata gag Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu 450 455 460	1392
cat cat ctt ttc cca aca atg ccc agg cat aat tta aac aaa ata gca His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala 465 470 475 480	1440
cct aga gtg gag gtg ttc tgt aag aaa cac ggt ctg gtg tac gaa gac Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp 485 490 495	1488
gta tct att gct acc ggc act tgc aag gtt ttg aaa gca ttg aag gaa Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu 500 505 510	1536
gtc gcg gag gct gcg gca gag cag cat gct acc acc agt taa Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser 515 520 525	1578

<210> 24  
 <211> 525  
 <212> PRT

&lt;213&gt; Physcomitrella patens

&lt;400&gt; 24

Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn  
 1 5 10 15

Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe  
 20 25 30

Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln  
 35 40 45

Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala  
 50 55 60

Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly  
 65 70 75 80

Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg  
 85 90 95

Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val  
 100 105 110

His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr  
 115 120 125

Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser  
 130 135 140

Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala  
 145 150 155 160

Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu  
 165 170 175

Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg  
 180 185 190

Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr  
 195 200 205

Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala  
 210 215 220

Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys  
 225 230 235 240

Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe  
 245 250 255

Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly  
 260 265 270

Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys  
 275 280 285

Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr  
 290 295 300

Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp  
 305 310 315 320

Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile  
 325 330 335

Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg  
 340 345 350

Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu  
 355 360 365

Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr  
 370 375 380

Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro  
 385 390 395 400

Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly  
 405 410 415

Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser  
 420 425 430

Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly  
 435 440 445

Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu  
 450 455 460

His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala  
 465 470 475 480

Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp  
 485 490 495

Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu  
 500 505 510

Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser  
 515 520 525

<210> 25  
 <211> 1332  
 <212> DNA  
 <213> *Caenorhabditis elegans*

<220>  
 <221> CDS  
 <222> (1)..(1332)  
 <223> Delta-6-Desaturase

<400> 25  
 atg gtc gtc gac aag aat gcc tcc ggg ctt cga atg aag gtc gat ggc 48  
 Met Val Val Asp Lys Asn Ala Ser Gly Leu Arg Met Lys Val Asp Gly  
 1 5 10 15  
 aaa tgg ctc tac ctt agc gag gaa ttg gtg aag aaa cat cca gga gga 96  
 Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His Pro Gly Gly  
 20 25 30  
 gct gtt att gaa caa tat aga aat tcg gat gct act cat att ttc cac 144  
 Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His Ile Phe His  
 35 40 45  
 gct ttc cac gaa gga tct tct cag gct tat aag caa ctt gac ctt ctg 192  
 Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu  
 50 55 60  
 aaa aag cac gga gag cac gat gaa ttc ctt gag aaa caa ttg gaa aag 240  
 Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys  
 65 70 75 80  
 aga ctt gac aaa gtt gat atc aat gta tca gca tat gat gtc agt gtt 288  
 Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val  
 85 90 95  
 gca caa gaa aag aaa atg gtt gaa tca ttc gaa aaa cta cga cag aag 336  
 Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys  
 100 105 110  
 ctt cat gat gat gga tta atg aaa gca aat gaa aca tat ttc ctg ttt 384  
 Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe  
 115 120 125  
 aaa gcg att tca aca ctt tca att atg gca ttt gca ttt tat ctt cag 432  
 Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln  
 130 135 140  
 tat ctt gga tgg tat att act tct gca tgt tta tta gca ctt gca tgg 480  
 Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp  
 145 150 155 160  
 caa caa ttc gga tgg tta aca cat gag ttc tgc cat caa cag cca aca 528  
 Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr  
 165 170 175  
 aag aac aga cct ttg aat gat act att tct ttg ttc ttt ggt aat ttc 576  
 Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe  
 180 185 190  
 tta caa gga ttt tca aga gat tgg tgg aag gac aag cat aac act cat 624  
 Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His  
 195 200 205  
 cac gct gcc aca aat gta att gat cat gac ggt gat atc gac ttg gca 672  
 His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala  
 210 215 220

46

cca ctt ttc gca ttt att cca gga gat ttg tgc aag tat aag gcc agc 720  
 Pro Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser  
 225 230 235 240

ttt gaa aaa gca att ctc aag att gta cca tat caa cat ctc tat ttc 768  
 Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe  
 245 250 255

acc gca atg ctt cca atg ctc cgt ttc tca tgg act ggt cag tca gtt 816  
 Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val  
 260 265 270

caa tgg gta ttc aaa gag aat caa atg gag tac aag gtc tat caa aga 864  
 Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg  
 275 280 285

aat gca ttc tgg gag caa gca aca att gtt gga cat tgg gct tgg gta 912  
 Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val  
 290 295 300

ttc tat caa ttg ttc tta tta cca aca tgg cca ctt cgg gtt gct tat 960  
 Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr  
 305 310 315 320

ttc att att tca caa atg gga gga ggc ctt ttg att gct cac gta gtc 1008  
 Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala His Val Val  
 325 330 335

act ttc aac cat aac tct gtt gat aag tat cca gcc aat tct cga att 1056  
 Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile  
 340 345 350

tta aac aac ttc gcc gct ctt caa att ttg acc aca cgc aac atg act 1104  
 Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr  
 355 360 365

cca tct cca ttc att gat tgg ctt tgg ggt gga ctc aat tat cag atc 1152  
 Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile  
 370 375 380

gag cac cac ttg ttc cca aca atg cca cgt tgc aat ctg aat gct tgc 1200  
 Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys  
 385 390 395 400

gtg aaa tat gtg aaa gaa tgg tgc aaa gag aat aat ctt cct tac ctc 1248  
 Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu  
 405 410 415

gtc gat gac tac ttt gac gga tat gca atg aat ttg caa caa ttg aaa 1296  
 Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln Gln Leu Lys  
 420 425 430

aat atg gct gag cac att caa gct aaa gct gcc taa 1332  
 Asn Met Ala Glu His Ile Gln Ala Lys Ala Ala  
 435 440

&lt;210&gt; 26

&lt;211&gt; 443

&lt;212&gt; PRT

&lt;213&gt; Caenorhabditis elegans

&lt;400&gt; 26

Met Val Val Asp Lys Asn Ala Ser Gly Leu Arg Met Lys Val Asp Gly  
 1 5 10 15

47

Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His Pro Gly Gly  
 20 25 30

Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His Ile Phe His  
 35 40 45

Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu  
 50 55 60

Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys  
 65 70 75 80

Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val  
 85 90 95

Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys  
 100 105 110

Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe  
 115 120 125

Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln  
 130 135 140

Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp  
 145 150 155 160

Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr  
 165 170 175

Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe  
 180 185 190

Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His  
 195 200 205

His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala  
 210 215 220

Pro Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser  
 225 230 235 240

Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe  
 245 250 255

Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val  
 260 265 270

Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg  
 275 280 285

Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val  
 290 295 300

Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr  
 305 310 315 320

Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala His Val Val  
 325 330 335

Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile  
 340 345 350

Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr  
 355 360 365

Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile  
 370 375 380

Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys  
 385 390 395 400

Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu  
 405 410 415

Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln Gln Leu Lys  
 420 425 430

Asn Met Ala Glu His Ile Gln Ala Lys Ala Ala  
 435 440

<210> 27  
 <211> 873  
 <212> DNA  
 <213> *Physcomitrella patens*

<220>  
 <221> CDS  
 <222> (1)..(873)  
 <223> Delta-6-Elongase

<400> 27  
 atg gag gtc gtg gag aga ttc tac ggt gag ttg gat ggg aag gtc tcg 48  
 Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser  
 1 5 10 15  
 cag ggc gtg aat gca ttg ctg ggt agt ttt ggg gtg gag ttg acg gat 96  
 Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp  
 20 25 30  
 acg ccc act acc aaa ggc ttg ccc ctc gtt gac agt ccc aca ccc atc 144  
 Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile  
 35 40 45  
 gtc ctc ggt gtt tct gta tac ttg act att gtc att gga ggg ctt ttg 192  
 Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu  
 50 55 60



## 49

tgg ata aag gcc agg gat ctg aaa ccg cgc gcc tcg gag cca ttt ttg	240
Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu	
65 70 75 80	
ctc caa gct ttg gtg ctt gtg cac aac ctg ttc tgt ttt gcg ctc agt	288
Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser	
85 90 95	
ctg tat atg tgc gtg ggc atc gct tat cag gct att acc tgg cgg tac	336
Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr	
100 105 110	
tct ctc tgg ggc aat gca tac aat cct aaa cat aaa gag atg gcg att	384
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile	
115 120 125	
ctg gta tac ttg ttc tac atg tct aag tac gtg gaa ttc atg gat acc	432
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr	
130 135 140	
gtt atc atg ata ctg aag cgc agc acc agg caa ata agc ttc ctc cac	480
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His	
145 150 155 160	
gtt tat cat cat tct tca att tcc ctc att tgg tgg gct att gct cat	528
Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His	
165 170 175	
cac gct cct ggc ggt gaa gca tat tgg tct gcg gct ctg aac tca gga	576
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly	
180 185 190	
gtg cat gtt ctc atg tat gcg tat tac ttc ttg gct gcc tgc ctt cga	624
Val His Val Leu Met Tyr Ala Tyr Phe Leu Ala Ala Cys Leu Arg	
195 200 205	
agt agc cca aag tta aaa aat aag tac ctt ttt tgg ggc agg tac ttg	672
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu	
210 215 220	
aca caa ttc caa atg ttc cag ttt atg ctg aac tta gtg cag gct tac	720
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr	
225 230 235 240	
tac gac atg aaa acg aat gcg cca tat cca caa tgg ctg atc aag att	768
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile	
245 250 255	
ttg ttc tac tac atg atc tcg ttg ctg ttt ctt ttc ggc aat ttt tac	816
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr	
260 265 270	
gta caa aaa tac atc aaa ccc tct gac gga aag caa aag gga gct aaa	864
Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys	
275 280 285	
act gag tga	873
Thr Glu	
290	

&lt;210&gt; 28

&lt;211&gt; 290

&lt;212&gt; PRT

&lt;213&gt; Physcomitrella patens

&lt;400&gt; 28

50

Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser  
 1 5 10 15  
 Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp  
 20 25 30  
 Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile  
 35 40 45  
 Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu  
 50 55 60  
 Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu  
 65 70 75 80  
 Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser  
 85 90 95  
 Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr  
 100 105 110  
 Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile  
 115 120 125  
 Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr  
 130 135 140  
 Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His  
 145 150 155 160  
 Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His  
 165 170 175  
 His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly  
 180 185 190  
 Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg  
 195 200 205  
 Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu  
 210 215 220  
 Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr  
 225 230 235 240  
 Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile  
 245 250 255  
 Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr  
 260 265 270

## 51

Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys  
 275 280 285

Thr Glu  
 290

<210> 29  
 <211> 1049  
 <212> DNA  
 <213> Thraustochytrium

<220>  
 <221> CDS  
 <222> (43)..(858)  
 <223> Delta-6-Elongase

<400> 29  
 gaattcggca cgagagcgcg cggagcggag acctcggccg cg atg atg gag ccg 54  
 Met Met Glu Pro  
 1

ctc gac agg tac agg gcg ctg gcg gag ctc gcc gcg agg tac gcc agc 102  
 Leu Asp Arg Tyr Arg Ala Leu Ala Glu Leu Ala Ala Arg Tyr Ala Ser  
 5 10 15 20

tcg gcg gcc ttc aag tgg caa gtc acg tac gac gcc aag gac agc ttc 150  
 Ser Ala Ala Phe Lys Trp Gln Val Thr Tyr Asp Ala Lys Asp Ser Phe  
 25 30 35

gtc ggg ccc ctg gga atc cgg gag ccg ctc ggg ctc ctg gtg ggc tcc 198  
 Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu Leu Val Gly Ser  
 40 45 50

gtg gtc ctc tac ctg agc ctg ctg gcc gtg gtc tac gcg ctg cgg aac 246  
 Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr Ala Leu Arg Asn  
 55 60 65

tac ctt ggc ggc ctc atg gcg ctc cgc agc gtg cat aac ctc ggg ctc 294  
 Tyr Leu Gly Gly Leu Met Ala Leu Arg Ser Val His Asn Leu Gly Leu  
 70 75 80

tgc ctc ttc tcg ggc gcc gtg tgg atc tac acg agc tac ctc atg atc 342  
 Cys Leu Phe Ser Gly Ala Val Trp Ile Tyr Thr Ser Tyr Leu Met Ile  
 85 90 95 100

cag gat ggg cac ttt cgc agc ctc gag gcg gca acg tgc gag ccg ctc 390  
 Gln Asp Gly His Phe Arg Ser Leu Glu Ala Ala Thr Cys Glu Pro Leu  
 105 110 115

aag cat ccg cac ttc cag ctc atc agc ttg ctc ttt gcg ctg tcc aag 438  
 Lys His Pro His Phe Gln Leu Ile Ser Leu Leu Phe Ala Leu Ser Lys  
 120 125 130

atc tgg gag tgg ttc gac acg gtg ctc ctc atc gtc aag ggc aac aag 486  
 Ile Trp Glu Trp Phe Asp Thr Val Leu Leu Ile Val Lys Gly Asn Lys  
 135 140 145

ctc cgc ttc ctg cac gtc ttg cac cac gcc acg acc ttt tgg ctc tac 534  
 Leu Arg Phe Leu His Val Leu His His Ala Thr Thr Phe Trp Leu Tyr  
 150 155 160

gcc atc gac cac atc ttt ctc tcg tcc atc aag tac ggc gtc gcg gtc 582  
 Ala Ile Asp His Ile Phe Leu Ser Ser Ile Lys Tyr Gly Val Ala Val  
 165 170 175 180

52

aat gct ttc atc cac acc gtc atg tac gcg cac tac ttc cgc cca ttc 630  
 Asn Ala Phe Ile His Thr Val Met Tyr Ala His Tyr Phe Arg Pro Phe  
 185 190 195  
 ccg aag ggc ttg cgc ccg ctt att acg cag ttg cag atc gtc cag ttc 678  
 Pro Lys Gly Leu Arg Pro Leu Ile Thr Gln Leu Gln Ile Val Gln Phe  
 200 205 210  
 att ttc agc atc ggc atc cat acc gcc att tac tgg cac tac gac tgc 726  
 Ile Phe Ser Ile Gly Ile His Thr Ala Ile Tyr Trp His Tyr Asp Cys  
 215 220 225  
 gag ccg ctc gtg cat acc cac ttt tgg gaa tac gtc acg ccc tac ctt 774  
 Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val Thr Pro Tyr Leu  
 230 235 240  
 ttc gtc gtg ccc ttc ctc atc ctc ttt ttc aat ttt tac ctg cag cag 822  
 Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe Tyr Leu Gln Gln  
 245 250 255 260  
 tac gtc ctc gcg ccc gca aaa acc aag aag gca tag ccacgtaaca 868  
 Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala  
 265 270  
 gtagaccagc agcgccgagc acgcgtgccg cggtatcgcg aagcacgaaa taaagaagat 928  
 catttgattc aacgaggcta cttgcggcca cgagaaaaaa aaaaaaaaaa aaaaaaaaaa 988  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1048  
 c 1049

<210> 30  
 <211> 271  
 <212> PRT  
 <213> Thraustochytrium

<400> 30

Met Met Glu Pro Leu Asp Arg Tyr Arg Ala Leu Ala Glu Leu Ala Ala  
 1 5 10 15  
 Arg Tyr Ala Ser Ser Ala Ala Phe Lys Trp Gln Val Thr Tyr Asp Ala  
 20 25 30  
 Lys Asp Ser Phe Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu  
 35 40 45  
 Leu Val Gly Ser Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr  
 50 55 60  
 Ala Leu Arg Asn Tyr Leu Gly Gly Leu Met Ala Leu Arg Ser Val His  
 65 70 75 80  
 Asn Leu Gly Leu Cys Leu Phe Ser Gly Ala Val Trp Ile Tyr Thr Ser  
 85 90 95  
 Tyr Leu Met Ile Gln Asp Gly His Phe Arg Ser Leu Glu Ala Ala Thr  
 100 105 110

## 53

Cys Glu Pro Leu Lys His Pro His Phe Gln Leu Ile Ser Leu Leu Phe  
 115 120 125

Ala Leu Ser Lys Ile Trp Glu Trp Phe Asp Thr Val Leu Leu Ile Val  
 130 135 140

Lys Gly Asn Lys Leu Arg Phe Leu His Val Leu His His Ala Thr Thr  
 145 150 155 160

Phe Trp Leu Tyr Ala Ile Asp His Ile Phe Leu Ser Ser Ile Lys Tyr  
 165 170 175

Gly Val Ala Val Asn Ala Phe Ile His Thr Val Met Tyr Ala His Tyr  
 180 185 190

Phe Arg Pro Phe Pro Lys Gly Leu Arg Pro Leu Ile Thr Gln Leu Gln  
 195 200 205

Ile Val Gln Phe Ile Phe Ser Ile Gly Ile His Thr Ala Ile Tyr Trp  
 210 215 220

His Tyr Asp Cys Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val  
 225 230 235 240

Thr Pro Tyr Leu Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe  
 245 250 255

Tyr Leu Gln Gln Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala  
 260 265 270

<210> 31  
 <211> 837  
 <212> DNA  
 <213> *Phytophthora infestans*

<220>  
 <221> CDS  
 <222> (1)..(837)  
 <223> Delta-6-Elongase

<400> 31  
 atg tcg act gag cta ctg cag agc tac tac gcg tgg gcc aac gcc acg 48  
 Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr  
 1 5 10 15  
 gag gcc aag ctg ctg gac tgg gtc gac cct gag ggc ggc tgg aag gtg 96  
 Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val  
 20 25 30  
 cat cct atg gca gac tac ccc cta gcc aac ttc tcc agc gtc tac gcc 144  
 His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala  
 35 40 45  
 atc tgc gtc gga tac ttg ctc ttc gta atc ttc ggc acg gcc ctg atg 192  
 Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met  
 50 55 60

## 54

aaa atg gga gtc ccc gcc atc aag acc agt cca tta cag ttt gtg tac 240  
 Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr  
 65 70 75 80

aac ccc atc caa gtc att gcc tgc tct tat atg tgc gtg gag gcc gcc 288  
 Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala  
 85 90 95

atc cag gcc tac cgc aac ggc tac acc gcc gcc ccg tgc aac gcc ttt 336  
 Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe  
 100 105 110

aag tcc gac gac ccc gtc atg ggc aac gtt ctg tac ctc ttc tat ctc 384  
 Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu  
 115 120 125

tcc aag atg ctc gac ctg tgc gac aca gtc ttc att atc cta gga aag 432  
 Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys  
 130 135 140

aag tgg aaa cag ctt tcc atc ttg cac gtg tac cac cac ctt acc gtg 480  
 Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val  
 145 150 155 160

ctt ttc gtc tac tat gtg acg ttc cgc gcc gct cag gac ggg gac tca 528  
 Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser  
 165 170 175

tat gct acc atc gtg ctc aac ggc ttc gtg cac acc atc atg tac act 576  
 Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr  
 180 185 190

tac tac ttc gtc agc gcc cac acg cgc aac att tgg tgg aag aag tac 624  
 Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr  
 195 200 205

ctc acg cgc att cag ctt atc cag ttc gtg acc atg aac gtg cag ggc 672  
 Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly  
 210 215 220

tac ctg acc tac tct cga cag tgc cca ggc atg cct cct aag gtg ccg 720  
 Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro  
 225 230 235 240

ctc atg tac ctt gtg tac gtg cag tca ctc ttc tgg ctc ttc atg aat 768  
 Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn  
 245 250 255

ttc tac att cgc gcg tac gtg ttc ggc ccc aag aaa ccg gcc gtg gag 816  
 Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu  
 260 265 270

gaa tcg aag aag aag ttg taa 837  
 Glu Ser Lys Lys Lys Leu  
 275

&lt;210&gt; 32

&lt;211&gt; 278

&lt;212&gt; PRT

<213> *Phytophthora infestans*

&lt;400&gt; 32

Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr  
 1 5 10 15

55

Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val  
 20 25 30

His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala  
 35 40 45

Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met  
 50 55 60

Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr  
 65 70 75 80

Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala  
 85 90 95

Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe  
 100 105 110

Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu  
 115 120 125

Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys  
 130 135 140

Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val  
 145 150 155 160

Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser  
 165 170 175

Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr  
 180 185 190

Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr  
 195 200 205

Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly  
 210 215 220

Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro  
 225 230 235 240

Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn  
 245 250 255

Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu  
 260 265 270

Glu Ser Lys Lys Lys Leu  
 275

<210> 33  
 <211> 954  
 <212> DNA  
 <213> Mortierella alpina

<220>  
 <221> CDS  
 <222> (1)..(954)  
 <223> Delta-6-Elongase

<400> 33  
 atg gcc gcc gca atc ttg gac aag gtc aac ttc ggc att gat cag ccc 48  
 Met Ala Ala Ala Ile Leu Asp Lys Val Asn Phe Gly Ile Asp Gln Pro  
 1 5 10 15

ttc gga atc aag ctc gac acc tac ttt gct cag gcc tat gaa ctc gtc 96  
 Phe Gly Ile Lys Leu Asp Thr Tyr Phe Ala Gln Ala Tyr Glu Leu Val  
 20 25 30

acc gga aag tcc atc gac tcc ttc gtc ttc cag gag ggc gtc acg cct 144  
 Thr Gly Lys Ser Ile Asp Ser Phe Val Phe Gln Glu Gly Val Thr Pro  
 35 40 45

ctc tcg acc cag aga gag gtc gcc atg tgg act atc act tac ttc gtc 192  
 Leu Ser Thr Gln Arg Glu Val Ala Met Trp Thr Ile Thr Tyr Phe Val  
 50 55 60

gtc atc ttt ggt ggt cgc cag atc atg aag agc cag gac gcc ttc aag 240  
 Val Ile Phe Gly Gly Arg Gln Ile Met Lys Ser Gln Asp Ala Phe Lys  
 65 70 75 80

ctc aag ccc ctc ttc atc ctc cac aac ttc ctc ctg acg atc gcg tcc 288  
 Leu Lys Pro Leu Phe Ile Leu His Asn Phe Leu Leu Thr Ile Ala Ser  
 85 90 95

gga tcg ctg ttg ctc ctg ttc atc gag aac ctg gtc ccc atc ctc gcc 336  
 Gly Ser Leu Leu Leu Leu Phe Ile Glu Asn Leu Val Pro Ile Leu Ala  
 100 105 110

aga aac gga ctt ttc tac gcc atc tgc gac gac ggt gcc tgg acc cag 384  
 Arg Asn Gly Leu Phe Tyr Ala Ile Cys Asp Asp Gly Ala Trp Thr Gln  
 115 120 125

cgc ctc gag ctc ctc tac tac ctc aac tac ctg gtc aag tac tgg gag 432  
 Arg Leu Glu Leu Leu Tyr Tyr Leu Asn Tyr Leu Val Lys Tyr Trp Glu  
 130 135 140

ttg gcc gac acc gtc ttt ttg gtc ctc aag aag aag cct ctt gag ttc 480  
 Leu Ala Asp Thr Val Phe Leu Val Leu Lys Lys Lys Pro Leu Glu Phe  
 145 150 155 160

ctg cac tac ttc cac cac tcg atg acc atg gtt ctc tgc ttt gtc cag 528  
 Leu His Tyr Phe His His Ser Met Thr Met Val Leu Cys Phe Val Gln  
 165 170 175

ctt gga gga tac act tca gtg tcc tgg gtc cct att acc ctc aac ttg 576  
 Leu Gly Gly Tyr Thr Ser Val Ser Trp Val Pro Ile Thr Leu Asn Leu  
 180 185 190

act gtc cac gtc ttc atg tac tac tac atg cgc tcc gct gcc ggt 624  
 Thr Val His Val Phe Met Tyr Tyr Tyr Met Arg Ser Ala Ala Gly  
 195 200 205

gtt cgc atc tgg tgg aag cag tac ttg acc act ctc cag atc gtc cag 672  
 Val Arg Ile Trp Trp Lys Gln Tyr Leu Thr Thr Leu Gln Ile Val Gln  
 210 215 220



57

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ttc gtt ctt gac ctc gga ttc atc tac ttc tgc gcc tac acc tac ttc      720
Phe Val Leu Asp Leu Gly Phe Ile Tyr Phe Cys Ala Tyr Thr Tyr Phe
225                230                235                240

gcc ttc acc tac ttc ccc tgg gct ccc aac gtc ggc aag tgc gcc ggt      768
Ala Phe Thr Tyr Phe Pro Trp Ala Pro Asn Val Gly Lys Cys Ala Gly
                245                250                255

acc gag ggt gct gct ctc ttt ggc tgc gga ctc ctc tcc agc tat ctc      816
Thr Glu Gly Ala Ala Leu Phe Gly Cys Gly Leu Leu Ser Ser Tyr Leu
                260                265                270

ttg ctc ttt atc aac ttc tac cgc att acc tac aat gcc aag gcc aag      864
Leu Leu Phe Ile Asn Phe Tyr Arg Ile Thr Tyr Asn Ala Lys Ala Lys
                275                280                285

gca gcc aag gag cgt gga agc aac ttt acc ccc aag act gtc aag tcc      912
Ala Ala Lys Glu Arg Gly Ser Asn Phe Thr Pro Lys Thr Val Lys Ser
                290                295                300

ggc gga tcg ccc aag aag ccc tcc aag agc aag cac atc taa      954
Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile
305                310                315

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<210> 34  
 <211> 317  
 <212> PRT  
 <213> Mortierella alpina

<400> 34

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Met Ala Ala Ala Ile Leu Asp Lys Val Asn Phe Gly Ile Asp Gln Pro
1                5                10                15

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Phe Gly Ile Lys Leu Asp Thr Tyr Phe Ala Gln Ala Tyr Glu Leu Val
                20                25                30

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Thr Gly Lys Ser Ile Asp Ser Phe Val Phe Gln Glu Gly Val Thr Pro
                35                40                45

```

```

Leu Ser Thr Gln Arg Glu Val Ala Met Trp Thr Ile Thr Tyr Phe Val
50                55                60

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```

Val Ile Phe Gly Gly Arg Gln Ile Met Lys Ser Gln Asp Ala Phe Lys
65                70                75                80

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```

Leu Lys Pro Leu Phe Ile Leu His Asn Phe Leu Leu Thr Ile Ala Ser
                85                90                95

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Gly Ser Leu Leu Leu Phe Ile Glu Asn Leu Val Pro Ile Leu Ala
                100                105                110

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Arg Asn Gly Leu Phe Tyr Ala Ile Cys Asp Asp Gly Ala Trp Thr Gln
                115                120                125

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Arg Leu Glu Leu Leu Tyr Tyr Leu Asn Tyr Leu Val Lys Tyr Trp Glu
130                135                140

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58

Leu Ala Asp Thr Val Phe Leu Val Leu Lys Lys Lys Pro Leu Glu Phe  
 145 150 155 160

Leu His Tyr Phe His His Ser Met Thr Met Val Leu Cys Phe Val Gln  
 165 170 175

Leu Gly Gly Tyr Thr Ser Val Ser Trp Val Pro Ile Thr Leu Asn Leu  
 180 185 190

Thr Val His Val Phe Met Tyr Tyr Tyr Tyr Met Arg Ser Ala Ala Gly  
 195 200 205

Val Arg Ile Trp Trp Lys Gln Tyr Leu Thr Thr Leu Gln Ile Val Gln  
 210 215 220

Phe Val Leu Asp Leu Gly Phe Ile Tyr Phe Cys Ala Tyr Thr Tyr Phe  
 225 230 235 240

Ala Phe Thr Tyr Phe Pro Trp Ala Pro Asn Val Gly Lys Cys Ala Gly  
 245 250 255

Thr Glu Gly Ala Ala Leu Phe Gly Cys Gly Leu Leu Ser Ser Tyr Leu  
 260 265 270

Leu Leu Phe Ile Asn Phe Tyr Arg Ile Thr Tyr Asn Ala Lys Ala Lys  
 275 280 285

Ala Ala Lys Glu Arg Gly Ser Asn Phe Thr Pro Lys Thr Val Lys Ser  
 290 295 300

Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile  
 305 310 315

<210> 35  
 <211> 957  
 <212> DNA  
 <213> Mortierella alpina

<220>  
 <221> CDS  
 <222> (1)..(957)  
 <223> Delta-6-Elongase

<400> 35  
 atg gag tgg att gcg cca ttc ctc cca tca aag atg ccg caa gat ctg 48  
 Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu  
 1 5 10 15  
 ttt atg gac ctt gcc acc gct atc ggt gtc cgg gcc gcg ccc tat gtc 96  
 Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val  
 20 25 30  
 gat cct ctc gag gcc gcg ctg gtg gcc cag gcc gag aag tac atc ccc 144  
 Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro  
 35 40 45

acg att gtc cat cac acg cgt ggg ttc ctg gtc gcg gtg gag tcg cct Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro 50 55 60	192
ttg gcc cgt gag ctg ccg ttg atg aac ccg ttc cac gtg ctg ttg atc Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile 65 70 75 80	240
gtg ctc gct tat ttg gtc acg gtc ttt gtg ggc atg cag atc atg aag Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys 85 90 95	288
aac ttt gag cgg ttc gag gtc aag acg ttt tcg ctc ctg cac aac ttt Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe 100 105 110	336
tgt ctg gtc tcg atc agc gcc tac atg tgc ggt ggg atc ctg tac gag Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu 115 120 125	384
gct tat cag gcc aac tat gga ctg ttt gag aac gct gct gat cat acc Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr 130 135 140	432
ttc aag ggt ctt cct atg gcc aag atg atc tgg ctc ttc tac ttc tcc Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser 145 150 155 160	480
aag atc atg gag ttt gtc gac acc atg atc atg gtc ctc aag aag aac Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn 165 170 175	528
aac cgc cag atc tcc ttc ttg cac gtt tac cac cac agc tcc atc ttc Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe 180 185 190	576
acc atc tgg tgg ttg gtc acc ttt gtt gca ccc aac ggt gaa gcc tac Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr 195 200 205	624
ttc tct gct gcg ttg aac tcg ttc atc cat gtg atc atg tac ggc tac Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr 210 215 220	672
tac ttc ttg tcg gcc ttg ggc ttc aag cag gtg tcg ttc atc aag ttc Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe 225 230 235 240	720
tac atc acg cgc tcg cag atg aca cag ttc tgc atg atg tcg gtc cag Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln 245 250 255	768
tct tcc tgg gac atg tac gcc atg aag gtc ctt ggc cgc ccc gga tac Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr 260 265 270	816
ccc ttc ttc atc acg gct ctg ctt tgg ttc tac atg tgg acc atg ctc Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu 275 280 285	864
ggt ctc ttc tac aac ttt tac aga aag aac gcc aag ttg gcc aag cag Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln 290 295 300	912
gcc aag gcc gac gct gcc aag gag aag gca agg aag ttg cag taa Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln 305 310 315	957

<210> 36  
 <211> 318  
 <212> PRT  
 <213> Mortierella alpina

<400> 36

Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu  
 1 5 10 15

Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val  
 20 25 30

Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro  
 35 40 45

Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro  
 50 55 60

Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile  
 65 70 75 80

Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys  
 85 90 95

Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe  
 100 105 110

Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu  
 115 120 125

Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr  
 130 135 140

Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser  
 145 150 155 160

Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn  
 165 170 175

Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe  
 180 185 190

Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr  
 195 200 205

Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr  
 210 215 220

Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe  
 225 230 235 240

Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln  
 245 250 255

Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr  
 260 265 270

Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu  
 275 280 285

Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln  
 290 295 300

Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln  
 305 310 315

<210> 37  
 <211> 867  
 <212> DNA  
 <213> Caenorhabditis elegans

<220>  
 <221> CDS  
 <222> (1)..(867)  
 <223> Delta-6-Elongase

<400> 37  
 atg gct cag cat ccg ctc gtt caa cgg ctt ctc gat gtc aaa ttc gac 48  
 Met Ala Gln His Pro Leu Val Gln Arg Leu Leu Asp Val Lys Phe Asp  
 1 5 10 15  
 acg aaa cga ttt gtg gct att gct act cat ggg cca aag aat ttc cct 96  
 Thr Lys Arg Phe Val Ala Ile Ala Thr His Gly Pro Lys Asn Phe Pro  
 20 25 30  
 gac gca gaa ggt cgc aag ttc ttt gct gat cac ttt gat gtt act att 144  
 Asp Ala Glu Gly Arg Lys Phe Phe Ala Asp His Phe Asp Val Thr Ile  
 35 40 45  
 cag gct tca atc ctg tac atg gtc gtt gtg ttc gga aca aaa tgg ttc 192  
 Gln Ala Ser Ile Leu Tyr Met Val Val Val Phe Gly Thr Lys Trp Phe  
 50 55 60  
 atg cgt aat cgt caa cca ttc caa ttg act att cca ctc aac atc tgg 240  
 Met Arg Asn Arg Gln Pro Phe Gln Leu Thr Ile Pro Leu Asn Ile Trp  
 65 70 75 80  
 aat ttc atc ctc gcc gca ttt tcc atc gca gga gct gtc aaa atg acc 288  
 Asn Phe Ile Leu Ala Ala Phe Ser Ile Ala Gly Ala Val Lys Met Thr  
 85 90 95  
 cca gag ttc ttt gga acc att gcc aac aaa gga att gtc gca tcc tac 336  
 Pro Glu Phe Phe Gly Thr Ile Ala Asn Lys Gly Ile Val Ala Ser Tyr  
 100 105 110  
 tgc aaa gtg ttt gat ttc acg aaa gga gag aat gga tac tgg gtg tgg 384  
 Cys Lys Val Phe Asp Phe Thr Lys Gly Glu Asn Gly Tyr Trp Val Trp  
 115 120 125  
 ctc ttc atg gct tcc aaa ctt ttc gaa ctt gtt gac acc atc ttc ttg 432  
 Leu Phe Met Ala Ser Lys Leu Phe Glu Leu Val Asp Thr Ile Phe Leu  
 130 135 140

## 62

gtt ctc cgt aaa cgt cca ctc atg ttc ctt cac tgg tat cac cat att 480  
 Val Leu Arg Lys Arg Pro Leu Met Phe Leu His Trp Tyr His His Ile  
 145 150 155 160  
 ctc acc atg atc tac gcc tgg tac tct cat cca ttg acc cca gga ttc 528  
 Leu Thr Met Ile Tyr Ala Trp Tyr Ser His Pro Leu Thr Pro Gly Phe  
 165 170 175  
 aac aga tac gga att tat ctt aac ttt gtc gtc cac gcc ttc atg tac 576  
 Asn Arg Tyr Gly Ile Tyr Leu Asn Phe Val Val His Ala Phe Met Tyr  
 180 185 190  
 tct tac tac ttc ctt cgc tcg atg aag att cgc gtg cca gga ttc atc 624  
 Ser Tyr Tyr Phe Leu Arg Ser Met Lys Ile Arg Val Pro Gly Phe Ile  
 195 200 205  
 gcc caa gct atc aca tct ctt caa atc gtt caa ttc atc atc tct tgc 672  
 Ala Gln Ala Ile Thr Ser Leu Gln Ile Val Gln Phe Ile Ile Ser Cys  
 210 215 220  
 gcc gtt ctt gct cat ctt ggt tat ctc atg cac ttc acc aat gcc aac 720  
 Ala Val Leu Ala His Leu Gly Tyr Leu Met His Phe Thr Asn Ala Asn  
 225 230 235 240  
 tgt gat ttc gag cca tca gta ttc aag ctc gca gtt ttc atg gac aca 768  
 Cys Asp Phe Glu Pro Ser Val Phe Lys Leu Ala Val Phe Met Asp Thr  
 245 250 255  
 aca tac ttg gct ctt ttc gtc aac ttc ttc ctc caa tca tat gtt ctc 816  
 Thr Tyr Leu Ala Leu Phe Val Asn Phe Phe Leu Gln Ser Tyr Val Leu  
 260 265 270  
 cgc gga gga aaa gac aag tac aag gca gtg cca aag aag aag aac aac 864  
 Arg Gly Gly Lys Asp Lys Tyr Lys Ala Val Pro Lys Lys Lys Asn Asn  
 275 280 285  
 taa 867  
 <210> 38  
 <211> 288  
 <212> PRT  
 <213> Caenorhabditis elegans  
 <400> 38  
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 1 5 10 15  
 Thr Lys Arg Phe Val Ala Ile Ala Thr His Gly Pro Lys Asn Phe Pro  
 20 25 30  
 Asp Ala Glu Gly Arg Lys Phe Phe Ala Asp His Phe Asp Val Thr Ile  
 35 40 45  
 Gln Ala Ser Ile Leu Tyr Met Val Val Val Phe Gly Thr Lys Trp Phe  
 50 55 60  
 Met Arg Asn Arg Gln Pro Phe Gln Leu Thr Ile Pro Leu Asn Ile Trp  
 65 70 75 80  
 Asn Phe Ile Leu Ala Ala Phe Ser Ile Ala Gly Ala Val Lys Met Thr  
 85 90 95

Pro Glu Phe Phe Gly Thr Ile Ala Asn Lys Gly Ile Val Ala Ser Tyr  
 100 105 110

Cys Lys Val Phe Asp Phe Thr Lys Gly Glu Asn Gly Tyr Trp Val Trp  
 115 120 125

Leu Phe Met Ala Ser Lys Leu Phe Glu Leu Val Asp Thr Ile Phe Leu  
 130 135 140

Val Leu Arg Lys Arg Pro Leu Met Phe Leu His Trp Tyr His His Ile  
 145 150 155 160

Leu Thr Met Ile Tyr Ala Trp Tyr Ser His Pro Leu Thr Pro Gly Phe  
 165 170 175

Asn Arg Tyr Gly Ile Tyr Leu Asn Phe Val Val His Ala Phe Met Tyr  
 180 185 190

Ser Tyr Tyr Phe Leu Arg Ser Met Lys Ile Arg Val Pro Gly Phe Ile  
 195 200 205

Ala Gln Ala Ile Thr Ser Leu Gln Ile Val Gln Phe Ile Ile Ser Cys  
 210 215 220

Ala Val Leu Ala His Leu Gly Tyr Leu Met His Phe Thr Asn Ala Asn  
 225 230 235 240

Cys Asp Phe Glu Pro Ser Val Phe Lys Leu Ala Val Phe Met Asp Thr  
 245 250 255

Thr Tyr Leu Ala Leu Phe Val Asn Phe Phe Leu Gln Ser Tyr Val Leu  
 260 265 270

Arg Gly Gly Lys Asp Lys Tyr Lys Ala Val Pro Lys Lys Lys Asn Asn  
 275 280 285

<210> 39  
 <211> 1626  
 <212> DNA  
 <213> *Euglena gracilis*

<220>  
 <221> CDS  
 <222> (1)..(1626)  
 <223> Delta-4-Desaturase

<400> 39  
 atg ttg gtg ctg ttt ggc aat ttc tat gtc aag caa tac tcc caa aag  
 Met Leu Val Leu Phe Gly Asn Phe Tyr Val Lys Gln Tyr Ser Gln Lys  
 1 5 10 15

aac ggc aag ccg gag aac gga gcc acc cct gag aac gga gcg aag ccg  
 Asn Gly Lys Pro Glu Asn Gly Ala Thr Pro Glu Asn Gly Ala Lys Pro

48

96

20	25	30	
caa cct tgc gag aac ggc acg gtg gaa aag cga gag aat gac acc gcc Gln Pro Cys Glu Asn Gly Thr Val Glu Lys Arg Glu Asn Asp Thr Ala 35 40 45			144
aac gtt cgg ccc acc cgt cca gct gga ccc ccg ccg gcc acg tac tac Asn Val Arg Pro Thr Arg Pro Ala Gly Pro Pro Pro Ala Thr Tyr Tyr 50 55 60			192
gac tcc ctg gca gtg tgc ggg cag ggc aag gag cgg ctg ttc acc acc Asp Ser Leu Ala Val Ser Gly Gln Gly Lys Glu Arg Leu Phe Thr Thr 65 70 75 80			240
gat gag gtg agg cgg cac atc ctc ccc acc gat ggc tgg ctg acg tgc Asp Glu Val Arg Arg His Ile Leu Pro Thr Asp Gly Trp Leu Thr Cys 85 90 95			288
cac gaa gga gtc tac gat gtc act gat ttc ctt gcc aag cac cct ggt His Glu Gly Val Tyr Asp Val Thr Asp Phe Leu Ala Lys His Pro Gly 100 105 110			336
ggc ggt gtc atc acg ctg ggc ctt gga agg gac tgc aca atc ctc atc Gly Gly Val Ile Thr Leu Gly Leu Gly Arg Asp Cys Thr Ile Leu Ile 115 120 125			384
gag tca tac cac cct gct ggg cgc ccg gac aag gtg atg gag aag tac Glu Ser Tyr His Pro Ala Gly Arg Pro Asp Lys Val Met Glu Lys Tyr 130 135 140			432
cgc att ggt acg ctg cag gac ccc aag acg ttc tat gct tgg gga gag Arg Ile Gly Thr Leu Gln Asp Pro Lys Thr Phe Tyr Ala Trp Gly Glu 145 150 155 160			480
tcc gat ttc tac cct gag ttg aag cgc cgg gcc ctt gca agg ctg aag Ser Asp Phe Tyr Pro Glu Leu Lys Arg Arg Ala Leu Ala Arg Leu Lys 165 170 175			528
gag gct ggt cag gcg cgg cgc ggc ggc ctt ggg gtg aag gcc ctc ctg Glu Ala Gly Gln Ala Arg Arg Gly Gly Leu Gly Val Lys Ala Leu Leu 180 185 190			576
gtg ctc acc ctc ttc ttc gtg tgc tgg tac atg tgg gtg gcc cac aag Val Leu Thr Leu Phe Phe Val Ser Trp Tyr Met Trp Val Ala His Lys 195 200 205			624
tcc ttc ctc tgg gcc gcc gtc tgg ggc ttc gcc ggc tcc cac gtc ggg Ser Phe Leu Trp Ala Ala Val Trp Gly Phe Ala Gly Ser His Val Gly 210 215 220			672
ctg agc atc cag cac gat ggc aac cac ggc gcg ttc agc cgc aac aca Leu Ser Ile Gln His Asp Gly Asn His Gly Ala Phe Ser Arg Asn Thr 225 230 235 240			720
ctg gtg aac cgc ctg gcg ggg tgg ggc atg gac ttg atc ggc gcg tgc Leu Val Asn Arg Leu Ala Gly Trp Gly Met Asp Leu Ile Gly Ala Ser 245 250 255			768
tcc acg gtg tgg gag tac cag cac gtc atc ggc cac cac cag tac acc Ser Thr Val Trp Glu Tyr Gln His Val Ile Gly His His Gln Tyr Thr 260 265 270			816
aac ctc gtg tgc gac acg cta ttc agt ctg cct gag aac gat ccg gac Asn Leu Val Ser Asp Thr Leu Phe Ser Leu Pro Glu Asn Asp Pro Asp 275 280 285			864
gtc ttc tcc agc tac ccg ctg atg cgc atg cac ccg gat acg gcg tgg Val Phe Ser Ser Tyr Pro Leu Met Arg Met His Pro Asp Thr Ala Trp			912



290	295	300	
cag ccg cac cac cgc ttc cag cac ctg ttc gcg ttc cca ctg ttc gcc Gln Pro His His Arg Phe Gln His Leu Phe Ala Phe Pro Leu Phe Ala 305 310 315 320			960
ctg atg aca atc agc aag gtg ctg acc agc gat ttc gct gtc tgc ctc Leu Met Thr Ile Ser Lys Val Leu Thr Ser Asp Phe Ala Val Cys Leu 325 330 335			1008
agc atg aag aag ggg tcc atc gac tgc tcc tcc agg ctc gtc cca ctg Ser Met Lys Lys Gly Ser Ile Asp Cys Ser Ser Arg Leu Val Pro Leu 340 345 350			1056
gag ggg cag ctg ctg ttc tgg ggg gcc aag ctg gcg aac ttc ctg ttg Glu Gly Gln Leu Leu Phe Trp Gly Ala Lys Leu Ala Asn Phe Leu Leu 355 360 365			1104
cag att gtg ttg cca tgc tac ctc cac ggg aca gct atg ggc ctg gcc Gln Ile Val Leu Pro Cys Tyr Leu His Gly Thr Ala Met Gly Leu Ala 370 375 380			1152
ctc ttc tct gtt gct cac ctt gtg tgc ggg gag tac ctc gcg atc tgc Leu Phe Ser Val Ala His Leu Val Ser Gly Glu Tyr Leu Ala Ile Cys 385 390 395 400			1200
ttc atc atc aac cac atc agc gag tct tgt gag ttt atg aat aca agc Phe Ile Ile Asn His Ile Ser Glu Ser Cys Glu Phe Met Asn Thr Ser 405 410 415			1248
ttt caa acc gcc gcc cgg agg aca gag atg ctt cag gca gca cat cag Phe Gln Thr Ala Ala Arg Arg Thr Glu Met Leu Gln Ala Ala His Gln 420 425 430			1296
gca gcg gag gcc aag aag gtg aag ccc acc cct cca ccg aac gat tgg Ala Ala Glu Ala Lys Lys Val Lys Pro Thr Pro Pro Pro Asn Asp Trp 435 440 445			1344
gct gtg aca cag gtc caa tgc tgc gtg aat tgg aga tca ggt ggc gtg Ala Val Thr Gln Val Gln Cys Cys Val Asn Trp Arg Ser Gly Gly Val 450 455 460			1392
ttg gcc aat cac ctc tct gga ggc ttg aac cac cag atc gag cat cat Leu Ala Asn His Leu Ser Gly Gly Leu Asn His Gln Ile Glu His His 465 470 475 480			1440
ctg ttc ccc agc atc tgc cat gcc aac tac ccc acc atc gcc cct gtt Leu Phe Pro Ser Ile Ser His Ala Asn Tyr Pro Thr Ile Ala Pro Val 485 490 495			1488
gtg aag gag gtg tgc gag gag tac ggg ttg ccg tac aag aat tac gtc Val Lys Glu Val Cys Glu Glu Tyr Gly Leu Pro Tyr Lys Asn Tyr Val 500 505 510			1536
acg ttc tgg gat gca gtc tgt ggc atg gtt cag cac ctc cgg ttg atg Thr Phe Trp Asp Ala Val Cys Gly Met Val Gln His Leu Arg Leu Met 515 520 525			1584
ggg gct cca ccg gtg cca acg aac ggg gac aaa aag tca taa Gly Ala Pro Pro Val Pro Thr Asn Gly Asp Lys Lys Ser 530 535 540			1626

&lt;210&gt; 40

&lt;211&gt; 541

&lt;212&gt; PRT

&lt;213&gt; Euglena gracilis

&lt;400&gt; 40

Met Leu Val Leu Phe Gly Asn Phe Tyr Val Lys Gln Tyr Ser Gln Lys  
 1 5 10 15

Asn Gly Lys Pro Glu Asn Gly Ala Thr Pro Glu Asn Gly Ala Lys Pro  
 20 25 30

Gln Pro Cys Glu Asn Gly Thr Val Glu Lys Arg Glu Asn Asp Thr Ala  
 35 40 45

Asn Val Arg Pro Thr Arg Pro Ala Gly Pro Pro Pro Ala Thr Tyr Tyr  
 50 55 60

Asp Ser Leu Ala Val Ser Gly Gln Gly Lys Glu Arg Leu Phe Thr Thr  
 65 70 75 80

Asp Glu Val Arg Arg His Ile Leu Pro Thr Asp Gly Trp Leu Thr Cys  
 85 90 95

His Glu Gly Val Tyr Asp Val Thr Asp Phe Leu Ala Lys His Pro Gly  
 100 105 110

Gly Gly Val Ile Thr Leu Gly Leu Gly Arg Asp Cys Thr Ile Leu Ile  
 115 120 125

Glu Ser Tyr His Pro Ala Gly Arg Pro Asp Lys Val Met Glu Lys Tyr  
 130 135 140

Arg Ile Gly Thr Leu Gln Asp Pro Lys Thr Phe Tyr Ala Trp Gly Glu  
 145 150 155 160

Ser Asp Phe Tyr Pro Glu Leu Lys Arg Arg Ala Leu Ala Arg Leu Lys  
 165 170 175

Glu Ala Gly Gln Ala Arg Arg Gly Gly Leu Gly Val Lys Ala Leu Leu  
 180 185 190

Val Leu Thr Leu Phe Phe Val Ser Trp Tyr Met Trp Val Ala His Lys  
 195 200 205

Ser Phe Leu Trp Ala Ala Val Trp Gly Phe Ala Gly Ser His Val Gly  
 210 215 220

Leu Ser Ile Gln His Asp Gly Asn His Gly Ala Phe Ser Arg Asn Thr  
 225 230 235 240

Leu Val Asn Arg Leu Ala Gly Trp Gly Met Asp Leu Ile Gly Ala Ser  
 245 250 255

Ser Thr Val Trp Glu Tyr Gln His Val Ile Gly His His Gln Tyr Thr  
 260 265 270

Asn Leu Val Ser Asp Thr Leu Phe Ser Leu Pro Glu Asn Asp Pro Asp  
 275 280 285

Val Phe Ser Ser Tyr Pro Leu Met Arg Met His Pro Asp Thr Ala Trp  
 290 295 300

Gln Pro His His Arg Phe Gln His Leu Phe Ala Phe Pro Leu Phe Ala  
 305 310 315 320

Leu Met Thr Ile Ser Lys Val Leu Thr Ser Asp Phe Ala Val Cys Leu  
 325 330 335

Ser Met Lys Lys Gly Ser Ile Asp Cys Ser Ser Arg Leu Val Pro Leu  
 340 345 350

Glu Gly Gln Leu Leu Phe Trp Gly Ala Lys Leu Ala Asn Phe Leu Leu  
 355 360 365

Gln Ile Val Leu Pro Cys Tyr Leu His Gly Thr Ala Met Gly Leu Ala  
 370 375 380

Leu Phe Ser Val Ala His Leu Val Ser Gly Glu Tyr Leu Ala Ile Cys  
 385 390 395 400

Phe Ile Ile Asn His Ile Ser Glu Ser Cys Glu Phe Met Asn Thr Ser  
 405 410 415

Phe Gln Thr Ala Ala Arg Arg Thr Glu Met Leu Gln Ala Ala His Gln  
 420 425 430

Ala Ala Glu Ala Lys Lys Val Lys Pro Thr Pro Pro Asn Asp Trp  
 435 440 445

Ala Val Thr Gln Val Gln Cys Cys Val Asn Trp Arg Ser Gly Gly Val  
 450 455 460

Leu Ala Asn His Leu Ser Gly Gly Leu Asn His Gln Ile Glu His His  
 465 470 475 480

Leu Phe Pro Ser Ile Ser His Ala Asn Tyr Pro Thr Ile Ala Pro Val  
 485 490 495

Val Lys Glu Val Cys Glu Glu Tyr Gly Leu Pro Tyr Lys Asn Tyr Val  
 500 505 510

Thr Phe Trp Asp Ala Val Cys Gly Met Val Gln His Leu Arg Leu Met  
 515 520 525

Gly Ala Pro Pro Val Pro Thr Asn Gly Asp Lys Lys Ser  
 530 535 540

<210> 41  
 <211> 1548  
 <212> DNA  
 <213> Thraustochytrium

<220>  
 <221> CDS  
 <222> (1)..(1548)  
 <223> Delta-4-Desaturase

<400> 41  
 atg acg gtc ggg ttt gac gaa acg gtg act atg gac acg gtc cgc aac 48  
 Met Thr Val Gly Phe Asp Glu Thr Val Thr Met Asp Thr Val Arg Asn  
 1 5 10 15  
 cac aac atg ccg gac gac gcc tgg tgc gcg atc cac ggc acc gtg tac 96  
 His Asn Met Pro Asp Asp Ala Trp Cys Ala Ile His Gly Thr Val Tyr  
 20 25 30  
 gac atc acc aag ttc agc aag gtg cac ccc ggc ggg gac atc atc atg 144  
 Asp Ile Thr Lys Phe Ser Lys Val His Pro Gly Gly Asp Ile Ile Met  
 35 40 45  
 ctg gcc gct ggc aag gag gcc acc atc ctg ttc gag acc tac cac atc 192  
 Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Ile  
 50 55 60  
 aag ggc gtc ccg gac gcg gtg ctg cgc aag tac aag gtc ggc aag ctc 240  
 Lys Gly Val Pro Asp Ala Val Leu Arg Lys Tyr Lys Val Gly Lys Leu  
 65 70 75 80  
 ccc cag ggc aag aag ggc gaa acg agc cac atg ccc acc ggc ctc gac 288  
 Pro Gln Gly Lys Lys Gly Glu Thr Ser His Met Pro Thr Gly Leu Asp  
 85 90 95  
 tcg gcc tcc tac tac tcg tgg gac agc gag ttt tac agg gtg ctc cgc 336  
 Ser Ala Ser Tyr Tyr Ser Trp Asp Ser Glu Phe Tyr Arg Val Leu Arg  
 100 105 110  
 gag cgc gtc gcc aag aag ctg gcc gag ccc ggc ctc atg cag cgc gcg 384  
 Glu Arg Val Ala Lys Lys Leu Ala Glu Pro Gly Leu Met Gln Arg Ala  
 115 120 125  
 cgc atg gag ctc tgg gcc aag gcg atc ttc ctc ctg gca ggt ttc tgg 432  
 Arg Met Glu Leu Trp Ala Lys Ala Ile Phe Leu Leu Ala Gly Phe Trp  
 130 135 140  
 ggc tcc ctt tac gcc atg tgc gtg cta gac ccg cac ggc ggt gcc atg 480  
 Gly Ser Leu Tyr Ala Met Cys Val Leu Asp Pro His Gly Gly Ala Met  
 145 150 155 160  
 gta gcc gcc gtt acg ctc ggc gtg ttc gct gcc ttt gtc gga act tgc 528  
 Val Ala Ala Val Thr Leu Gly Val Phe Ala Ala Phe Val Gly Thr Cys  
 165 170 175  
 atc cag cac gac ggc agc cac ggc gcc ttc tcc aag tcg cga ttc atg 576  
 Ile Gln His Asp Gly Ser His Gly Ala Phe Ser Lys Ser Arg Phe Met  
 180 185 190  
 aac aag gcg gcg ggc tgg acc ctc gac atg atc ggc gcg agt gcg atg 624  
 Asn Lys Ala Ala Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Met  
 195 200 205  
 acc tgg gag atg cag cac gtt ctt ggc cac cac ccg tac acc aac ctc 672  
 Thr Trp Glu Met Gln His Val Leu Gly His His Pro Tyr Thr Asn Leu

210	215	220	
atc gag atg gag aac ggt ttg gcc aag gtc aag ggc gcc gac gtc gac			720
Ile Glu Met Glu Asn Gly Leu Ala Lys Val Lys Gly Ala Asp Val Asp			
225	230	235	240
ccg aag aag gtc gac cag gag agc gac ccg gac gtc ttc agt acg tac			768
Pro Lys Lys Val Asp Gln Glu Ser Asp Pro Asp Val Phe Ser Thr Tyr			
245	250		255
ccg atg ctt cgc ctg cac ccg tgg cac cgc cag cgg ttt tac cac aag			816
Pro Met Leu Arg Leu His Pro Trp His Arg Gln Arg Phe Tyr His Lys			
260	265		270
ttc cag cac ctg tac gcc ccg ttt atc ttt ggg tct atg acg att aac			864
Phe Gln His Leu Tyr Ala Pro Phe Ile Phe Gly Ser Met Thr Ile Asn			
275	280		285
aag gtg att tcc cag gat gtc ggg gtt gtg ctg cgc aag cgc ctg ttc			912
Lys Val Ile Ser Gln Asp Val Gly Val Val Leu Arg Lys Arg Leu Phe			
290	295		300
cag atc gac gcc aac tgc cgg tat ggc agc ccc tgg tac gtg gcc cgc			960
Gln Ile Asp Ala Asn Cys Arg Tyr Gly Ser Pro Trp Tyr Val Ala Arg			
305	310		315
ttc tgg atc atg aag ctc ctc acc acg ctc tac atg gtg gcg ctt ccc			1008
Phe Trp Ile Met Lys Leu Leu Thr Thr Leu Tyr Met Val Ala Leu Pro			
325	330		335
atg tac atg cag ggg cct gct cag ggc ttg aag ctt ttc ttc atg gcc			1056
Met Tyr Met Gln Gly Pro Ala Gln Gly Leu Lys Leu Phe Phe Met Ala			
340	345		350
cac ttc acc tgc gga gag gtc ctc gcc acc atg ttt att gtc aac cac			1104
His Phe Thr Cys Gly Glu Val Leu Ala Thr Met Phe Ile Val Asn His			
355	360		365
atc atc gag ggc gtc agc tac gct tcc aag gac gcg gtc aag ggc gtc			1152
Ile Ile Glu Gly Val Ser Tyr Ala Ser Lys Asp Ala Val Lys Gly Val			
370	375		380
atg gct ccg ccg cgc act gtg cac ggt gtc acc ccg atg cag gtg acg			1200
Met Ala Pro Pro Arg Thr Val His Gly Val Thr Pro Met Gln Val Thr			
385	390		395
caa aag gcg ctc agt gcg gcc gag tcg gcc aag tcg gac gcc gac aag			1248
Gln Lys Ala Leu Ser Ala Ala Glu Ser Ala Lys Ser Asp Ala Asp Lys			
405	410		415
acg acc atg atc ccc ctc aac gac tgg gcc gct gtg cag tgc cag acc			1296
Thr Thr Met Ile Pro Leu Asn Asp Trp Ala Ala Val Gln Cys Gln Thr			
420	425		430
tct gtg aac tgg gct gtc ggg tcg tgg ttt tgg aac cac ttt tcg gcc			1344
Ser Val Asn Trp Ala Val Gly Ser Trp Phe Trp Asn His Phe Ser Gly			
435	440		445
ggc ctc aac cac cag att gag cac cac tgc ttc ccc caa aac ccc cac			1392
Gly Leu Asn His Gln Ile Glu His His Cys Phe Pro Gln Asn Pro His			
450	455		460
acg gtc aac gtc tac atc tcg gcc atc gtc aag gag acc tgc gaa gaa			1440
Thr Val Asn Val Tyr Ile Ser Gly Ile Val Lys Glu Thr Cys Glu Glu			
465	470		475
tac gcc gtg ccg tac cag gct gag atc agc ctc ttc tct gcc tat ttc			1488
Tyr Gly Val Pro Tyr Gln Ala Glu Ile Ser Leu Phe Ser Ala Tyr Phe			

485

490

495

aag atg ctg tcg cac ctc cgc acg ctc ggc aac gag gac ctc acg gcc 1536  
Lys Met Leu Ser His Leu Arg Thr Leu Gly Asn Glu Asp Leu Thr Ala  
500 505 510

tgg tcc acg tga  
 Trp Ser Thr  
 515

<210>	42
<211>	515
<212>	PRT
<213>	Thraustochytrium

<400> 42

Met Thr Val Gly Phe Asp Glu Thr Val Thr Met Asp Thr Val Arg Asn  
1 5 10 15

His Asn Met Pro Asp Asp Ala Trp Cys Ala Ile His Gly Thr Val Tyr  
20 25 30

Asp Ile Thr Lys Phe Ser Lys Val His Pro Gly Gly Asp Ile Ile Met  
35 40 45

Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Ile  
50 55 60

Lys Gly Val Pro Asp Ala Val Leu Arg Lys Tyr Lys Val Gly Lys Leu  
65 70 75 80

Pro Gln Gly Lys Lys Gly Glu Thr Ser His Met Pro Thr Gly Leu Asp  
85 90 95

Ser Ala Ser Tyr Tyr Ser Trp Asp Ser Glu Phe Tyr Arg Val Leu Arg  
100 105 110

Glu Arg Val Ala Lys Lys Leu Ala Glu Pro Gly Leu Met Gln Arg Ala.  
115 120 125

Arg Met Glu Leu Trp Ala Lys Ala Ile Phe Leu Leu Ala Gly Phe Trp  
130 135 140

Gly Ser Leu Tyr Ala Met Cys Val Leu Asp Pro His Gly Gly Ala Met  
145 150 155 160

Val Ala Ala Val Thr Leu Gly Val Phe Ala Ala Phe Val Gly Thr Cys  
165 170 175

Ile Gln His Asp Gly Ser His Gly Ala Phe Ser Lys Ser Arg Phe Met  
180 185 190

Asn Lys Ala Ala Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Met  
195 200 205

Thr Trp Glu Met Gln His Val Leu Gly His His Pro Tyr Thr Asn Leu  
 210 215 220

Ile Glu Met Glu Asn Gly Leu Ala Lys Val Lys Gly Ala Asp Val Asp  
 225 230 235 240

Pro Lys Lys Val Asp Gln Glu Ser Asp Pro Asp Val Phe Ser Thr Tyr  
 245 250 255

Pro Met Leu Arg Leu His Pro Trp His Arg Gln Arg Phe Tyr His Lys  
 260 265 270

Phe Gln His Leu Tyr Ala Pro Phe Ile Phe Gly Ser Met Thr Ile Asn  
 275 280 285

Lys Val Ile Ser Gln Asp Val Gly Val Val Leu Arg Lys Arg Leu Phe  
 290 295 300

Gln Ile Asp Ala Asn Cys Arg Tyr Gly Ser Pro Trp Tyr Val Ala Arg  
 305 310 315 320

Phe Trp Ile Met Lys Leu Leu Thr Thr Leu Tyr Met Val Ala Leu Pro  
 325 330 335

Met Tyr Met Gln Gly Pro Ala Gln Gly Leu Lys Leu Phe Phe Met Ala  
 340 345 350

His Phe Thr Cys Gly Glu Val Leu Ala Thr Met Phe Ile Val Asn His  
 355 360 365

Ile Ile Glu Gly Val Ser Tyr Ala Ser Lys Asp Ala Val Lys Gly Val  
 370 375 380

Met Ala Pro Pro Arg Thr Val His Gly Val Thr Pro Met Gln Val Thr  
 385 390 395 400

Gln Lys Ala Leu Ser Ala Ala Glu Ser Ala Lys Ser Asp Ala Asp Lys  
 405 410 415

Thr Thr Met Ile Pro Leu Asn Asp Trp Ala Ala Val Gln Cys Gln Thr  
 420 425 430

Ser Val Asn Trp Ala Val Gly Ser Trp Phe Trp Asn His Phe Ser Gly  
 435 440 445

Gly Leu Asn His Gln Ile Glu His His Cys Phe Pro Gln Asn Pro His  
 450 455 460

Thr Val Asn Val Tyr Ile Ser Gly Ile Val Lys Glu Thr Cys Glu Glu  
 465 470 475 480

Tyr Gly Val Pro Tyr Gln Ala Glu Ile Ser Leu Phe Ser Ala Tyr Phe  
 485 490 495

Lys Met Leu Ser His Leu Arg Thr Leu Gly Asn Glu Asp Leu Thr Ala  
 500 505 510

Trp Ser Thr  
 515

<210> 43  
 <211> 960  
 <212> DNA  
 <213> *Thalassiosira pseudonana*

<220>  
 <221> CDS  
 <222> (1)..(960)  
 <223> Delta-5-Elongase

<400> 43  
 atg gtg ttg tac aat gtg gcg caa gtg ctg ctc aat ggg tgg acg gtg 48  
 Met Val Leu Tyr Asn Val Ala Gln Val Leu Leu Asn Gly Trp Thr Val  
 1 5 10 15  
 tat gcg att gtg gat gcg gtg atg aat aga gac cat ccg ttt att gga 96  
 Tyr Ala Ile Val Asp Ala Val Met Asn Arg Asp His Pro Phe Ile Gly  
 20 25 30  
 agt aga agt ttg gtt ggg gcg gcg ttg cat agt ggg agc tcg tat gcg 144  
 Ser Arg Ser Leu Val Gly Ala Ala Leu His Ser Gly Ser Ser Tyr Ala  
 35 40 45  
 gtg tgg gtt cat tat tgt gat aag tat ttg gag ttc ttt gat acg tat 192  
 Val Trp Val His Tyr Cys Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr  
 50 55 60  
 ttt atg gtg ttg agg ggg aaa atg gac cag atg gta ctt ggt gaa gtt 240  
 Phe Met Val Leu Arg Gly Lys Met Asp Gln Met Val Leu Gly Glu Val  
 65 70 75 80  
 ggt ggc agt gtg tgg tgt ggc gtt gga tat atg gat atg gag aag atg 288  
 Gly Gly Ser Val Trp Cys Gly Val Gly Tyr Met Asp Met Glu Lys Met  
 85 90 95  
 ata cta ctc agc ttt gga gtg cat cgg tct gct cag gga acg ggg aag 336  
 Ile Leu Leu Ser Phe Gly Val His Arg Ser Ala Gln Gly Thr Gly Lys  
 100 105 110  
 gct ttc acc aac aac gtt acc aat cca cat ctc acg ctt cca cct cat 384  
 Ala Phe Thr Asn Asn Val Thr Asn Pro His Leu Thr Leu Pro Pro His  
 115 120 125  
 tct aca aaa aca aaa aaa cag gtc tcc ttc ctc cac atc tac cac cac 432  
 Ser Thr Lys Thr Lys Lys Gln Val Ser Phe Leu His Ile Tyr His His  
 130 135 140  
 acg acc ata gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggt 480  
 Thr Thr Ile Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly  
 145 150 155 160  
 gga gac att tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc 528  
 Gly Asp Ile Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu



165	170	175	
atg tat tcc tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg			576
Met Tyr Ser Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp			
180	185	190	
aaa cga tac ctg act caa gct caa tta ttg caa ttc aca agt gtg gtg			624
Lys Arg Tyr Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val			
195	200	205	
gtt tat acg ggg tgt acg ggt tat act cat tac tat cat acg aag cat			672
Val Tyr Thr Gly Cys Thr Thr Tyr Thr His Tyr Tyr His Thr Lys His			
210	215	220	
gga gcg gat gag aca cag cct agt tta gga acg tat tat ttc tgt tgt			720
Gly Ala Asp Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys			
225	230	235	240
gga gtg cag gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc			768
Gly Val Gln Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile			
245	250	255	
ttt tat aaa cga tcc tat tcg aag aag aac aag tca gga gga aag gat			816
Phe Tyr Lys Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp			
260	265	270	
agc aag aag aat gat gat ggg aat aat gag gat caa tgt cac aag gct			864
Ser Lys Lys Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala			
275	280	285	
atg aag gat ata tcg gag ggt gcg aag gag gtt gtg ggg cat gca gcg			912
Met Lys Asp Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala			
290	295	300	
aag gat gct gga aag ttg gtg gct acg aga gta agg tgt aag gtg taa			960
Lys Asp Ala Gly Lys Leu Val Ala Thr Arg Val Arg Cys Lys Val			
305	310	315	

<210> 44  
 <211> 319  
 <212> PRT  
 <213> Thalassiosira pseudonana

<400> 44

Met Val Leu Tyr Asn Val Ala Gln Val Leu Leu Asn Gly Trp Thr Val  
 1 5 10 15

Tyr Ala Ile Val Asp Ala Val Met Asn Arg Asp His Pro Phe Ile Gly  
 20 25 30

Ser Arg Ser Leu Val Gly Ala Ala Leu His Ser Gly Ser Ser Tyr Ala  
 35 40 45

Val Trp Val His Tyr Cys Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr  
 50 55 60

Phe Met Val Leu Arg Gly Lys Met Asp Gln Met Val Leu Gly Glu Val  
 65 70 75 80

Gly Gly Ser Val Trp Cys Gly Val Gly Tyr Met Asp Met Glu Lys Met  
 85 90 95

Ile Leu Leu Ser Phe Gly Val His Arg Ser Ala Gln Gly Thr Gly Lys  
 100 105 110

Ala Phe Thr Asn Asn Val Thr Asn Pro His Leu Thr Leu Pro Pro His  
 115 120 125

Ser Thr Lys Thr Lys Lys Gln Val Ser Phe Leu His Ile Tyr His His  
 130 135 140

Thr Thr Ile Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly  
 145 150 155 160

Gly Asp Ile Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu  
 165 170 175

Met Tyr Ser Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp  
 180 185 190

Lys Arg Tyr Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val  
 195 200 205

Val Tyr Thr Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His  
 210 215 220

Gly Ala Asp Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys  
 225 230 235 240

Gly Val Gln Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile  
 245 250 255

Phe Tyr Lys Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp  
 260 265 270

Ser Lys Lys Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala  
 275 280 285

Met Lys Asp Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala  
 290 295 300

Lys Asp Ala Gly Lys Leu Val Ala Thr Arg Val Arg Cys Lys Val  
 305 310 315

<210> 45  
 <211> 819  
 <212> DNA  
 <213> *Thalassiosira pseudonana*

<220>  
 <221> CDS  
 <222> (1)..(819)  
 <223> Delta-5-Elongase

<400> 45  
 atg gac gcc tac aac gct gca atg gat aag atc ggt gcc gcc atc atc 48  
 Met Asp Ala Tyr Asn Ala Ala Met Asp Lys Ile Gly Ala Ala Ile Ile  
 1 5 10 15  
 gat tgg tct gat ccc gat gga aag ttc cgt gcc gat aga gag gac tgg 96  
 Asp Trp Ser Asp Pro Asp Gly Lys Phe Arg Ala Asp Arg Glu Asp Trp  
 20 25 30  
 tgg ctc tgc gac ttc cgt agc gcc atc acc atc gcc ctc atc tac atc 144  
 Trp Leu Cys Asp Phe Arg Ser Ala Ile Thr Ile Ala Leu Ile Tyr Ile  
 35 40 45  
 gcc ttc gtc atc ctc ggt tcc gcc gtc atg caa tcc ctc ccc gca atg 192  
 Ala Phe Val Ile Leu Gly Ser Ala Val Met Gln Ser Leu Pro Ala Met  
 50 55 60  
 gat ccc tac ccc atc aaa ttc ctc tac aac gtc tcc caa atc ttc ctt 240  
 Asp Pro Tyr Pro Ile Lys Phe Leu Tyr Asn Val Ser Gln Ile Phe Leu  
 65 70 75 80  
 tgt gcc tac atg act gtc gag gcg gga ttt ttg gcc tac cgc aat gga 288  
 Cys Ala Tyr Met Thr Val Glu Ala Gly Phe Leu Ala Tyr Arg Asn Gly  
 85 90 95  
 tat acc gtc atg cct tgc aat cat ttc aat gtg aat gat cct ccc gtg 336  
 Tyr Thr Val Met Pro Cys Asn His Phe Asn Val Asn Asp Pro Pro Val  
 100 105 110  
 gcg aat ctt ctt tgg ttg ttt tat att tcc aag gtg tgg gac ttt tgg 384  
 Ala Asn Leu Leu Trp Leu Phe Tyr Ile Ser Lys Val Trp Asp Phe Trp  
 115 120 125  
 gat acc att ttc att gtg ttg ggg aag aag tgg cgt caa tta tct ttc 432  
 Asp Thr Ile Phe Ile Val Leu Gly Lys Lys Trp Arg Gln Leu Ser Phe  
 130 135 140  
 ttg cat gta tac cat cac acc acc atc ttt cta ttc tat tgg ctg aat 480  
 Leu His Val Tyr His His Thr Thr Ile Phe Leu Phe Tyr Trp Leu Asn  
 145 150 155 160  
 gcc aat gtc ttg tac gat ggt gac atc ttc ctt acc atc ttg ctc aat 528  
 Ala Asn Val Leu Tyr Asp Gly Asp Ile Phe Leu Thr Ile Leu Leu Asn  
 165 170 175  
 gga ttc atc cac acg gtg atg tac acg tat tac ttc atc tgt atg cat 576  
 Gly Phe Ile His Thr Val Met Tyr Thr Tyr Tyr Phe Ile Cys Met His  
 180 185 190  
 acc aaa gat tcc aag acg ggc aag agt ctt cct ata tgg tgg aag tcg 624  
 Thr Lys Asp Ser Lys Thr Gly Lys Ser Leu Pro Ile Trp Trp Lys Ser  
 195 200 205  
 agt ttg acg gcg ttt cag ttg ttg caa ttc act atc atg atg agt cag 672  
 Ser Leu Thr Ala Phe Gln Leu Leu Gln Phe Thr Ile Met Met Ser Gln  
 210 215 220  
 gct acc tac ctt gtc ttc cac ggg tgt gat aag gtg tcg ctt cgt atc 720  
 Ala Thr Tyr Leu Val Phe His Gly Cys Asp Lys Val Ser Leu Arg Ile  
 225 230 235 240  
 acg att gtg tac ttt gtg tcc ctt ttg agt ttg ttc ttc ctt ttt gct 768  
 Thr Ile Val Tyr Phe Val Ser Leu Leu Ser Leu Phe Phe Leu Phe Ala  
 245 250 255  
 cag ttc ttt gtg caa tca tac atg gca ccc aaa aag aag aag agt gct 816  
 Gln Phe Phe Val Gln Ser Tyr Met Ala Pro Lys Lys Lys Lys Ser Ala

260 265 270 819

tag

<210> 46  
 <211> 272  
 <212> PRT  
 <213> *Thalassiosira pseudonana*

<400> 46

Met Asp Ala Tyr Asn Ala Ala Met Asp Lys Ile Gly Ala Ala Ile Ile  
 1 5 10 15

Asp Trp Ser Asp Pro Asp Gly Lys Phe Arg Ala Asp Arg Glu Asp Trp  
 20 25 30

Trp Leu Cys Asp Phe Arg Ser Ala Ile Thr Ile Ala Leu Ile Tyr Ile  
 35 40 45

Ala Phe Val Ile Leu Gly Ser Ala Val Met Gln Ser Leu Pro Ala Met  
 50 55 60

Asp Pro Tyr Pro Ile Lys Phe Leu Tyr Asn Val Ser Gln Ile Phe Leu  
 65 70 75 80

Cys Ala Tyr Met Thr Val Glu Ala Gly Phe Leu Ala Tyr Arg Asn Gly  
 85 90 95

Tyr Thr Val Met Pro Cys Asn His Phe Asn Val Asn Asp Pro Pro Val  
 100 105 110

Ala Asn Leu Leu Trp Leu Phe Tyr Ile Ser Lys Val Trp Asp Phe Trp  
 115 120 125

Asp Thr Ile Phe Ile Val Leu Gly Lys Lys Trp Arg Gln Leu Ser Phe  
 130 135 140

Leu His Val Tyr His His Thr Thr Ile Phe Leu Phe Tyr Trp Leu Asn  
 145 150 155 160

Ala Asn Val Leu Tyr Asp Gly Asp Ile Phe Leu Thr Ile Leu Leu Asn  
 165 170 175

Gly Phe Ile His Thr Val Met Tyr Thr Tyr Tyr Phe Ile Cys Met His  
 180 185 190

Thr Lys Asp Ser Lys Thr Gly Lys Ser Leu Pro Ile Trp Trp Lys Ser  
 195 200 205

Ser Leu Thr Ala Phe Gln Leu Leu Gln Phe Thr Ile Met Met Ser Gln  
 210 215 220

Ala Thr Tyr Leu Val Phe His Gly Cys Asp Lys Val Ser Leu Arg Ile  
 225 230 235 240

Thr Ile Val Tyr Phe Val Ser Leu Leu Ser Leu Phe Phe Leu Phe Ala  
 245 250 255

Gln Phe Phe Val Gln Ser Tyr Met Ala Pro Lys Lys Lys Lys Ser Ala  
 260 265 270

<210> 47  
 <211> 936  
 <212> DNA  
 <213> Crypthecodinium cohnii

<220>  
 <221> CDS  
 <222> (1)..(936)  
 <223> Delta-5-Elongase

<400> 47  
 atg tct gcc ttc atg act ctc cca cag gct ctc tcc gat gtg acc tcg 48  
 Met Ser Ala Phe Met Thr Leu Pro Gln Ala Leu Ser Asp Val Thr Ser  
 1 5 10 15  
 gcc ttg gtc acg ctg gga aag gat gtc tcc agc cct tca gct ttt caa 96  
 Ala Leu Val Thr Leu Gly Lys Asp Val Ser Ser Pro Ser Ala Phe Gln  
 20 25 30  
 gct gtc act ggc ttc tgc agg gag cag tgg ggg att ccg aca gta ttc 144  
 Ala Val Thr Gly Phe Cys Arg Glu Gln Trp Gly Ile Pro Thr Val Phe  
 35 40 45  
 tgc ctg ggc tac ttg gcc atg gtc tac gcg gcc aga aga ccc ctc ccg 192  
 Cys Leu Gly Tyr Leu Ala Met Val Tyr Ala Ala Arg Arg Pro Leu Pro  
 50 55 60  
 cag cac ggc tac atg gtt gcg gtg gac cgt tgc ttc gct gct tgg aac 240  
 Gln His Gly Tyr Met Val Ala Val Asp Arg Cys Phe Ala Ala Trp Asn  
 65 70 75 80  
 ttg gct ctc tct gtc ttc agc act tgg ggc ttc tac cac atg gct gtc 288  
 Leu Ala Leu Ser Val Phe Ser Thr Trp Gly Phe Tyr His Met Ala Val  
 85 90 95  
 ggg ctc tac aac atg aca gag acg agg ggc ttg caa ttc acc atc tgc 336  
 Gly Leu Tyr Asn Met Thr Glu Thr Arg Gly Leu Gln Phe Thr Ile Cys  
 100 105 110  
 ggt tcg act ggg gag ctc gtg cag aac ctt cag act ggc cca acc gct 384  
 Gly Ser Thr Gly Glu Leu Val Gln Asn Leu Gln Thr Gly Pro Thr Ala  
 115 120 125  
 ctg gcg ctc tgc ctc ttc tgc ttc agc aag atc ccc gag ttg atg gac 432  
 Leu Ala Leu Cys Leu Phe Cys Phe Ser Lys Ile Pro Glu Leu Met Asp  
 130 135 140  
 acg gtg ttt ctc atc ctg aag gcc aag aag gtc cgc ttc ttg cag tgg 480  
 Thr Val Phe Leu Ile Leu Lys Ala Lys Lys Val Arg Phe Leu Gln Trp  
 145 150 155 160  
 tac cac cat gcc aca gtc atg ctc ttc tgt tgg ctc gcc ctc gcg acg 528  
 Tyr His His Ala Thr Val Met Leu Phe Cys Trp Leu Ala Leu Ala Thr  
 165 170 175

gag tac act cct ggc ttg tgg ttt gcg gcg acg aac tac ttc gtg cac 576  
 Glu Tyr Thr Pro Gly Leu Trp Phe Ala Ala Thr Asn Tyr Phe Val His  
 180 185 190

tcc atc atg tac atg tac ttc ttc ctc atg acc ttc aag tcg gcc gcg 624  
 Ser Ile Met Tyr Met Tyr Phe Phe Leu Met Thr Phe Lys Ser Ala Ala  
 195 200 205

aag gtg gtg aag ccc atc gcc cct ctc atc aca gtt atc cag att gct 672  
 Lys Val Val Lys Pro Ile Ala Pro Leu Ile Thr Val Ile Gln Ile Ala  
 210 215 220

cag atg gtc tgg ggc ctc atc gtc aac ggc atc gcc atc acc acc ttc 720  
 Gln Met Val Trp Gly Leu Ile Val Asn Gly Ile Ala Ile Thr Thr Phe  
 225 230 235 240

ttc acg act ggt gcc tgc cag atc cag tct gtg act gtg tat tcg gcc 768  
 Phe Thr Thr Gly Ala Cys Gln Ile Gln Ser Val Thr Val Tyr Ser Ala  
 245 250 255

atc atc atg tac gct tcg tac ttc tac ctg ttc tcc cag ctc ttc ttc 816  
 Ile Ile Met Tyr Ala Ser Tyr Phe Tyr Leu Phe Ser Gln Leu Phe Phe  
 260 265 270

gag gcc cat ggt gcc gct ggc aag aac aag aag aag ttg acc cgc gag 864  
 Glu Ala His Gly Ala Ala Gly Lys Asn Lys Lys Lys Leu Thr Arg Glu  
 275 280 285

ctc tct cga aaa atc tcg gag gct ctc ctg aac acc ggt gac gag gtt 912  
 Leu Ser Arg Lys Ile Ser Glu Ala Leu Leu Asn Thr Gly Asp Glu Val  
 290 295 300

tcc aag cac ctg aag gtg aat tga 936  
 Ser Lys His Leu Lys Val Asn  
 305 310

<210> 48  
 <211> 311  
 <212> PRT  
 <213> Crypthecodinium cohnii  
 <400> 48

Met Ser Ala Phe Met Thr Leu Pro Gln Ala Leu Ser Asp Val Thr Ser  
 1 5 10 15

Ala Leu Val Thr Leu Gly Lys Asp Val Ser Ser Pro Ser Ala Phe Gln  
 20 25 30

Ala Val Thr Gly Phe Cys Arg Glu Gln Trp Gly Ile Pro Thr Val Phe  
 35 40 45

Cys Leu Gly Tyr Leu Ala Met Val Tyr Ala Ala Arg Arg Pro Leu Pro  
 50 55 60

Gln His Gly Tyr Met Val Ala Val Asp Arg Cys Phe Ala Ala Trp Asn  
 65 70 75 80

Leu Ala Leu Ser Val Phe Ser Thr Trp Gly Phe Tyr His Met Ala Val  
 85 90 95

79

Gly Leu Tyr Asn Met Thr Glu Thr Arg Gly Leu Gln Phe Thr Ile Cys  
 100 105 110

Gly Ser Thr Gly Glu Leu Val Gln Asn Leu Gln Thr Gly Pro Thr Ala  
 115 120 125

Leu Ala Leu Cys Leu Phe Cys Phe Ser Lys Ile Pro Glu Leu Met Asp  
 130 135 140

Thr Val Phe Leu Ile Leu Lys Ala Lys Lys Val Arg Phe Leu Gln Trp  
 145 150 155 160

Tyr His His Ala Thr Val Met Leu Phe Cys Trp Leu Ala Leu Ala Thr  
 165 170 175

Glu Tyr Thr Pro Gly Leu Trp Phe Ala Ala Thr Asn Tyr Phe Val His  
 180 185 190

Ser Ile Met Tyr Met Tyr Phe Phe Leu Met Thr Phe Lys Ser Ala Ala  
 195 200 205

Lys Val Val Lys Pro Ile Ala Pro Leu Ile Thr Val Ile Gln Ile Ala  
 210 215 220

Gln Met Val Trp Gly Leu Ile Val Asn Gly Ile Ala Ile Thr Thr Phe  
 225 230 235 240

Phe Thr Thr Gly Ala Cys Gln Ile Gln Ser Val Thr Val Tyr Ser Ala  
 245 250 255

Ile Ile Met Tyr Ala Ser Tyr Phe Tyr Leu Phe Ser Gln Leu Phe Phe  
 260 265 270

Glu Ala His Gly Ala Ala Gly Lys Asn Lys Lys Lys Leu Thr Arg Glu  
 275 280 285

Leu Ser Arg Lys Ile Ser Glu Ala Leu Leu Asn Thr Gly Asp Glu Val  
 290 295 300

Ser Lys His Leu Lys Val Asn  
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<220>  
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<400> 49

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act ttg aac cac gac ttc tcc agc gtc gag cca ttc aaa gtc gtg acg Thr Leu Asn His Asp Phe Ser Ser Val Glu Pro Phe Lys Val Val Thr 20 25 30	96
cag ttc tgc agg gac cag tgg gcg atc ccg aca gtc ttt tgc atc ggt Gln Phe Cys Arg Asp Gln Trp Ala Ile Pro Thr Val Phe Cys Ile Gly 35 40 45	144
tac ttg gca atg gtc tac gcc acg cga aga cct atc gcg aag cac ccc Tyr Leu Ala Met Val Tyr Ala Thr Arg Arg Pro Ile Ala Lys His Pro 50 55 60	192
tac atg tct ctc gtg gat cgc tgc ttt gcg gcc tgg aac ttg ggc ctc Tyr Met Ser Leu Val Asp Arg Cys Phe Ala Ala Trp Asn Leu Gly Leu 65 70 75 80	240
tcg ctc ttc agt tgc tgg ggc ttc tac cac atg gca gtg gga ctc tcc Ser Leu Phe Ser Cys Trp Gly Phe Tyr His Met Ala Val Gly Leu Ser 85 90 95	288
cac acc act tgg aat ttc ggg ctc cag ttc acc atc tgc ggc agc acc His Thr Thr Trp Asn Phe Gly Leu Gln Phe Thr Ile Cys Gly Ser Thr 100 105 110	336
acg gag ctt gtg aat ggc ttc cag aag ggc ccg gcg gcc ctc gcc ctc Thr Glu Leu Val Asn Gly Phe Gln Lys Gly Pro Ala Ala Leu Ala Leu 115 120 125	384
atc ctg ttc tgc ttc tcc aag atc ccg gag ttg ggc gac acc gtc ttc Ile Leu Phe Cys Phe Ser Lys Ile Pro Glu Leu Gly Asp Thr Val Phe 130 135 140	432
ttg atc ttg aag gga aag aag gtc cgc ttc ttg cag tgg tac cac cac Leu Ile Leu Lys Gly Lys Lys Val Arg Phe Leu Gln Trp Tyr His His 145 150 155 160	480
acg acc gtg atg ctc ttc tgt tgg atg gcc ttg gcg act gag tac act Thr Thr Val Met Leu Phe Cys Trp Met Ala Leu Ala Thr Glu Tyr Thr 165 170 175	528
cct gga ttg tgg ttc gcg gcc acg aac tac ttc gtg cac tcc atc atg Pro Gly Leu Trp Phe Ala Ala Thr Asn Tyr Phe Val His Ser Ile Met 180 185 190	576
tac atg tac ttc ttc ctc atg acc ttc aag acg gcc gcc ggc atc atc Tyr Met Tyr Phe Phe Leu Met Thr Phe Lys Thr Ala Ala Gly Ile Ile 195 200 205	624
aag ccc atc gcg cct ctc atc acc atc atc cag atc tcc cag atg gtc Lys Pro Ile Ala Pro Leu Ile Thr Ile Ile Gln Ile Ser Gln Met Val 210 215 220	672
tgg ggc ttg gtc gtg aac gcc atc gcc gtc ggc acc ttc ttc acc aca Trp Gly Leu Val Val Asn Ala Ile Ala Val Gly Thr Phe Phe Thr Thr 225 230 235 240	720
ggc aac tgc cag atc cag gca gtg aca gtc tac tcc gcc atc gtg atg Gly Asn Cys Gln Ile Gln Ala Val Thr Val Tyr Ser Ala Ile Val Met 245 250 255	768
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864

912

927

<400> 50

Thr Leu Asn His Asp Phe Ser Ser Val Glu Pro Phe Lys Val Val Thr  
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Gln Phe Cys Arg Asp Gln Trp Ala Ile Pro Thr Val Phe Cys Ile Gly  
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Tyr Leu Ala Met Val Tyr Ala Thr Arg Arg Pro Ile Ala Lys His Pro  
50 55 60

Tyr Met Ser Leu Val Asp Arg Cys Phe Ala Ala Trp Asn Leu Gly Leu  
65 70 75 80

Ser Leu Phe Ser Cys Trp Gly Phe Tyr His Met Ala Val Gly Leu Ser  
85 90 95

His Thr Thr Trp Asn Phe Gly Leu Gln Phe Thr Ile Cys Gly Ser Thr  
100 105 110

Thr Glu Leu Val Asn Gly Phe Gln Lys Gly Pro Ala Ala Leu Ala Leu  
115 120 125

Ile Leu Phe Cys Phe Ser Lys Ile Pro Glu Leu Gly Asp Thr Val Phe  
130 135 140

Leu Ile Leu Lys Gly Lys Lys Val Arg Phe Leu Gln Trp Tyr His His  
145 150 155 160

Thr Thr Val Met Leu Phe Cys Trp Met Ala Leu Ala Thr Glu Tyr Thr  
165 170 175

Pro Gly Leu Trp Phe Ala Ala Thr Asn Tyr Phe Val His Ser Ile Met  
180 185 190

Tyr Met Tyr Phe Phe Leu Met Thr Phe Lys Thr Ala Ala Gly Ile Ile  
195 200 205

Lys Pro Ile Ala Pro Leu Ile Thr Ile Ile Gln Ile Ser Gln Met Val  
210 215 220

Trp Gly Leu Val Val Asn Ala Ile Ala Val Gly Thr Phe Phe Thr Thr  
225 230 235 240

Gly Asn Cys Gln Ile Gln Ala Val Thr Val Tyr Ser Ala Ile Val Met  
245 250 255

Tyr Ala Ser Tyr Phe Tyr Leu Phe Gly Gln Leu Phe Phe Glu Ala Gln  
260 265 270

Gly Ser Ala Gly Lys Asp Lys Lys Lys Leu Ala Arg Glu Leu Ser Arg  
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Lys Val Ser Arg Ala Leu Thr Ala Thr Gly Glu Glu Val Ser Lys His  
290 295 300

Met Lys Val Asn  
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gag aat gga gat aaa agg aca gac cca tgg cta ctg gtc tac tcc cct 96  
Glu Asn Gly Asp Lys Arg Thr Asp Pro Trp Leu Leu Val Tyr Ser Pro  
20 25 30  
  
atg cca gtg gcc att ata ttc ctc ctc tat ctt ggt gtg gtc tgg gct 144  
Met Pro Val Ala Ile Ile Phe Leu Leu Tyr Leu Gly Val Val Trp Ala  
35 40 45  
  
ggg ccc aag ctg atg aaa cgc agg gaa cca gtt gat ctc aag gct gta 192  
Gly Pro Lys Leu Met Lys Arg Arg Glu Pro Val Asp Leu Lys Ala Val  
50 55 60  
  
ctc att gtc tac aac ttc gcc atg gtc tgc ctg tct gtc tac atg ttc 240  
Leu Ile Val Tyr Asn Phe Ala Met Val Cys Leu Ser Val Tyr Met Phe  
65 70 75 80  
  
cat gag ttc ttg gtc acg tcc ttg ctg tct aac tac agt tac ctg tgt 288  
His Glu Phe Leu Val Thr Ser Leu Leu Ser Asn Tyr Ser Tyr Leu Cys  
85 90 95

caa cct gtg gat tac agc act agt cca ctg gcg atg agg atg gcc aaa 336  
 Gln Pro Val Asp Tyr Ser Thr Ser Pro Leu Ala Met Arg Met Ala Lys  
 100 105 110

gta tgc tgg tgg ttt ttc ttc tcc aag gtc ata gaa ttg gct gac acg 384  
 Val Cys Trp Trp Phe Phe Phe Ser Lys Val Ile Glu Leu Ala Asp Thr  
 115 120 125

gtg ttc ttc atc ctg agg aag aag aac agt cag ctg act ttc ctg cat 432  
 Val Phe Phe Ile Leu Arg Lys Lys Asn Ser Gln Leu Thr Phe Leu His  
 130 135 140

gtc tat cac cat ggc acc atg atc ttc aac tgg tgg gca ggg gtc aag 480  
 Val Tyr His His Gly Thr Met Ile Phe Asn Trp Trp Ala Gly Val Lys  
 145 150 155 160

tat ctg gct gga ggc caa tcg ttc ttc atc ggc ctg ctc aat acc ttt 528  
 Tyr Leu Ala Gly Gln Ser Phe Phe Ile Gly Leu Leu Asn Thr Phe  
 165 170 175

gtg cac atc gtg atg tac tct tac tac gga ctg gct gcc ctg ggg cct 576  
 Val His Ile Val Met Tyr Ser Tyr Tyr Gly Leu Ala Ala Leu Gly Pro  
 180 185 190

cac acg cag aag tac tta tgg tgg aag cgc tat ctg acc tca ctg cag 624  
 His Thr Gln Lys Tyr Leu Trp Trp Lys Arg Tyr Leu Thr Ser Leu Gln  
 195 200 205

ctg ctc cag ttt gtc ctg ttg acc act cac act ggc tac aac ctc ttc 672  
 Leu Leu Gln Phe Val Leu Leu Thr Thr His Thr Gly Tyr Asn Leu Phe  
 210 215 220

act gag tgt gac ttc ccg gac tcc atg aac gct gtg gtg ttt gcc tac 720  
 Thr Glu Cys Asp Phe Pro Asp Ser Met Asn Ala Val Val Phe Ala Tyr  
 225 230 235 240

tgt gtc agt ctc att gct ctc ttc agc aac ttc tac tat cag agc tac 768  
 Cys Val Ser Leu Ile Ala Leu Phe Ser Asn Phe Tyr Tyr Gln Ser Tyr  
 245 250 255

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<210> 52  
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 <213> Oncorhynchus mykiss

<400> 52

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 20 25 30

Met Pro Val Ala Ile Ile Phe Leu Leu Tyr Leu Gly Val Val Trp Ala  
 35 40 45

Gly Pro Lys Leu Met Lys Arg Arg Glu Pro Val Asp Leu Lys Ala Val  
 50 55 60

84

Leu Ile Val Tyr Asn Phe Ala Met Val Cys Leu Ser Val Tyr Met Phe  
65 70 75 80

His Glu Phe Leu Val Thr Ser Leu Leu Ser Asn Tyr Ser Tyr Leu Cys  
85 90 95

Gln Pro Val Asp Tyr Ser Thr Ser Pro Leu Ala Met Arg Met Ala Lys  
100 105 110

Val Cys Trp Trp Phe Phe Phe Ser Lys Val Ile Glu Leu Ala Asp Thr  
115 120 125

Val Phe Phe Ile Leu Arg Lys Lys Asn Ser Gln Leu Thr Phe Leu His  
130 135 140

Val Tyr His His Gly Thr Met Ile Phe Asn Trp Trp Ala Gly Val Lys  
145 150 155 160

Tyr Leu Ala Gly Gly Gln Ser Phe Phe Ile Gly Leu Leu Asn Thr Phe  
165 170 175

Val His Ile Val Met Tyr Ser Tyr Tyr Gly Leu Ala Ala Leu Gly Pro  
180 185 190

His Thr Gln Lys Tyr Leu Trp Trp Lys Arg Tyr Leu Thr Ser Leu Gln  
195 200 205

Leu Leu Gln Phe Val Leu Leu Thr Thr His Thr Gly Tyr Asn Leu Phe  
210 215 220

Thr Glu Cys Asp Phe Pro Asp Ser Met Asn Ala Val Val Phe Ala Tyr  
225 230 235 240

Cys Val Ser Leu Ile Ala Leu Phe Ser Asn Phe Tyr Tyr Gln Ser Tyr  
245 250 255

Leu Asn Arg Lys Ser Lys Lys Thr  
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<210> 53  
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<220>  
<221> CDS  
<222> (1)..(885)  
<223> Delta-5-Elongase

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Met Glu Thr Phe Asn Tyr Lys Leu Asn Met Tyr Ile Asp Ser Trp Met  
1 5 10 15

48

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cct cca acc ttt gca cta aca gtc atg tac ctg ctg atc gta tgg atg Pro Pro Thr Phe Ala Leu Thr Val Met Tyr Leu Leu Ile Val Trp Met 35 40 45	144
ggg ccc aag tac atg aga cac aga cag ccg gtg tct tgc cgg ggt ctc Gly Pro Lys Tyr Met Arg His Arg Gln Pro Val Ser Cys Arg Gly Leu 50 55 60	192
ctc ttg gtc tac aat ctg ggc ctc acg atc ttg tcc ttc tat atg ttc Leu Leu Val Tyr Asn Leu Gly Leu Thr Ile Leu Ser Phe Tyr Met Phe 65 70 75 80	240
tat gag atg gtg tct gct gtg tgg cac ggg gat tat aac ttc ttt tgc Tyr Glu Met Val Ser Ala Val Trp His Gly Asp Tyr Asn Phe Phe Cys 85 90 95	288
caa gac aca cac agt gca gga gaa acc gat acc aag atc ata aat gtg Gln Asp Thr His Ser Ala Gly Glu Thr Asp Thr Lys Ile Ile Asn Val 100 105 110	336
ctg tgg tgg tac tac ttc tcc aag ctc ata gag ttt atg gat acc ttc Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe 115 120 125	384
ttc ttc atc ctg cgg aag aac aac cat caa atc acg ttt ctg cac atc Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Phe Leu His Ile 130 135 140	432
tac cac cat gct agc atg ctc aac atc tgg tgg ttc gtc atg aac tgg Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp 145 150 155 160	480
gtg ccc tgt ggt cac tcc tac ttt ggt gcc tcc ctg aac agc ttc atc Val Pro Cys Gly His Ser Tyr Phe Gly Ala Ser Leu Asn Ser Phe Ile 165 170 175	528
cat gtc ctg atg tac tct tac tat ggg ctc tct gct gtc ccg gcc ttg His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ala Val Pro Ala Leu 180 185 190	576
cgg ccc tat cta tgg tgg aag aaa tac atc aca caa gta cag ctg att Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Val Gln Leu Ile 195 200 205	624
cag ttc ttt ttg acc atg tcc cag acg ata tgt gca gtc att tgg cca Gln Phe Phe Leu Thr Met Ser Gln Thr Ile Cys Ala Val Ile Trp Pro 210 215 220	672
tgt gat ttc ccc aga ggg tgg ctg tat ttc cag ata ttc tat gtc atc Cys Asp Phe Pro Arg Gly Trp Leu Tyr Phe Gln Ile Phe Tyr Val Ile 225 230 235 240	720
aca ctt att gcc ctt ttc tca aac ttc tac att cag act tac aag aaa Thr Leu Ile Ala Leu Phe Ser Asn Phe Tyr Ile Gln Thr Tyr Lys Lys 245 250 255	768
cac ctt gtt tca caa aag aag gag tat cat cag aat ggc tct gtt gct His Leu Val Ser Gln Lys Lys Glu Tyr His Gln Asn Gly Ser Val Ala 260 265 270	816
tca ttg aat ggc cat gtg aat ggg gtg aca ccc acg gaa acc att aca Ser Leu Asn Gly His Val Asn Gly Val Thr Pro Thr Glu Thr Ile Thr 275 280 285	864

cac agg aaa gtg agg ggg gac  
His Arg Lys Val Arg Gly Asp  
290 295

<210> 54  
<211> 295  
<212> PRT  
<213> Oncorhynchus mykiss

<400> 54

Met Glu Thr Phe Asn Tyr Lys Leu Asn Met Tyr Ile Asp Ser Trp Met  
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20 25 30

Pro Pro Thr Phe Ala Leu Thr Val Met Tyr Leu Leu Ile Val Trp Met  
35 40 45

Gly Pro Lys Tyr Met Arg His Arg Gln Pro Val Ser Cys Arg Gly Leu  
50 55 60

Leu Leu Val Tyr Asn Leu Gly Leu Thr Ile Leu Ser Phe Tyr Met Phe  
65 70 75 80

Tyr Glu Met Val Ser Ala Val Trp His Gly Asp Tyr Asn Phe Phe Cys  
85 90 95

Gln Asp Thr His Ser Ala Gly Glu Thr Asp Thr Lys Ile Ile Asn Val  
100 105 110

Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe  
115 120 125

Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Phe Leu His Ile  
130 135 140

Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp  
145 150 155 160

Val Pro Cys Gly His Ser Tyr Phe Gly Ala Ser Leu Asn Ser Phe Ile  
165 170 175

His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ala Val Pro Ala Leu  
180 185 190

Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Val Gln Leu Ile  
195 200 205

Gln Phe Phe Leu Thr Met Ser Gln Thr Ile Cys Ala Val Ile Trp Pro  
210 215 220

Cys Asp Phe Pro Arg Gly Trp Leu Tyr Phe Gln Ile Phe Tyr Val Ile  
 225 230 235 240

Thr Leu Ile Ala Leu Phe Ser Asn Phe Tyr Ile Gln Thr Tyr Lys Lys  
 245 250 255

His Leu Val Ser Gln Lys Lys Glu Tyr His Gln Asn Gly Ser Val Ala  
 260 265 270

Ser Leu Asn Gly His Val Asn Gly Val Thr Pro Thr Glu Thr Ile Thr  
 275 280 285

His Arg Lys Val Arg Gly Asp  
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<210> 55  
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 acaataaaga ttctacaata ctagctttta tgggttatgaa gaggaataat tggcagtaac 180  
 ctggccccac aaaccttcaa atgaacgaat caaattaaca accataggat gataatgcga 240  
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 cctctatact ttaacgtcaa ggagaaaaaa ccccggtatcg gactactagc agctgtaata 480  
 cgactcacta taggggaatat taagcttaca ta atg gag act ttt aat tat aaa 533  
 Met Glu Thr Phe Asn Tyr Lys  
 1 5  
 cta aac atg tac ata gac tca tgg atg ggt ccc aga gat gag cgg gta 581  
 Leu Asn Met Tyr Ile Asp Ser Trp Met Gly Pro Arg Asp Glu Arg Val  
 10 15 20  
 cag gga tgg ctg ctt ctg gac aac tac cct cca acc ttt gca cta aca 629  
 Gln Gly Trp Leu Leu Leu Asp Asn Tyr Pro Pro Thr Phe Ala Leu Thr  
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 gtc atg tac ctg ctg atc gta tgg atg ggg ccc aag tac atg aga cac 677  
 Val Met Tyr Leu Leu Ile Val Trp Met Gly Pro Lys Tyr Met Arg His  
 40 45 50 55  
 aga cag ccg gtg tct tgc cgg ggt ctc ctc ttg gtc tac aat ctg ggc 725  
 Arg Gln Pro Val Ser Cys Arg Gly Leu Leu Leu Val Tyr Asn Leu Gly  
 60 65 70

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tgg cac ggg gat tat aac ttc ttt tgc caa gac aca cac agt gca gga Trp His Gly Asp Tyr Asn Phe Phe Cys Gln Asp Thr His Ser Ala Gly 90 95 100	821
gaa acc gat acc aag atc ata aat gtg ctg tgg tgg tac tac ttc tcc Glu Thr Asp Thr Lys Ile Ile Asn Val Leu Trp Trp Tyr Tyr Phe Ser 105 110 115	869
aag ctc ata gag ttt atg gat acc ttc ttc ttc atc ctg cgg aag aac Lys Leu Ile Glu Phe Met Asp Thr Phe Phe Phe Ile Leu Arg Lys Asn 120 125 130 135	917
aac cat caa atc acg ttt ctg cac atc tac cac cat gct agc atg ctc Asn His Gln Ile Thr Phe Leu His Ile Tyr His His Ala Ser Met Leu 140 145 150	965
aac atc tgg tgg ttc gtc atg aac tgg gtg ccc tgt ggt cac tcc tac Asn Ile Trp Trp Phe Val Met Asn Trp Val Pro Cys Gly His Ser Tyr 155 160 165	1013
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aac ttc tac att cag act tac aag aaa cac ctt gtt tca caa aag aag Asn Phe Tyr Ile Gln Thr Tyr Lys Lys His Leu Val Ser Gln Lys Lys 250 255 260	1301
gag tat cat cag aat ggc tct gtt gct tca ttg aat ggc cat gtg aat Glu Tyr His Gln Asn Gly Ser Val Ala Ser Leu Asn Gly His Val Asn 265 270 275	1349
ggg gtg aca ccc acg gaa acc att aca cac agg aaa gtg agg ggg gac Gly Val Thr Pro Thr Glu Thr Ile Thr His Arg Lys Val Arg Gly Asp 280 285 290 295	1397
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<400> 56

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Pro Pro Thr Phe Ala Leu Thr Val Met Tyr Leu Leu Ile Val Trp Met  
35 40 45

Gly Pro Lys Tyr Met Arg His Arg Gln Pro Val Ser Cys Arg Gly Leu  
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Leu Leu Val Tyr Asn Leu Gly Leu Thr Ile Leu Ser Phe Tyr Met Phe  
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Tyr Glu Met Val Ser Ala Val Trp His Gly Asp Tyr Asn Phe Phe Cys  
85 90 95

Gln Asp Thr His Ser Ala Gly Glu Thr Asp Thr Lys Ile Ile Asn Val  
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Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe  
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Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Phe Leu His Ile  
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Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp  
 145 150 155 160

Val Pro Cys Gly His Ser Tyr Phe Gly Ala Ser Leu Asn Ser Phe Ile  
 165 170 175

His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ala Val Pro Ala Leu  
 180 185 190

Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Val Gln Leu Ile  
 195 200 205

Gln Phe Phe Leu Thr Met Ser Gln Thr Ile Cys Ala Val Ile Trp Pro  
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Cys Asp Phe Pro Arg Gly Trp Leu Tyr Phe Gln Ile Phe Tyr Val Ile  
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Thr Leu Ile Ala Leu Phe Ser Asn Phe Tyr Ile Gln Thr Tyr Lys Lys  
 245 250 255

His Leu Val Ser Gln Lys Lys Glu Tyr His Gln Asn Gly Ser Val Ala  
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Arg Glu Pro Val Asp Leu Lys Ala Val Leu Ile Val Tyr Asn Phe Ala	
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Met Val Cys Leu Ser Val Tyr Met Phe His Glu Phe Leu Val Thr Ser	
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Ser Pro Leu Ala Met Arg Met Ala Lys Val Cys Trp Trp Phe Phe Phe	
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Ser Lys Val Ile Glu Leu Ala Asp Thr Val Phe Phe Ile Leu Arg Lys	
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Tyr Tyr Gly Leu Ala Ala Leu Gly Pro His Thr Gln Lys Tyr Leu Trp	
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Trp Lys Arg Tyr Leu Thr Ser Leu Gln Leu Leu Gln Phe Val Leu Leu	
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&lt;211&gt; 264

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<213> *Oncorhynchus mykiss*

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Gly Pro Lys Leu Met Lys Arg Arg Glu Pro Val Asp Leu Lys Ala Val  
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Leu Ile Val Tyr Asn Phe Ala Met Val Cys Leu Ser Val Tyr Met Phe  
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His Glu Phe Leu Val Thr Ser Leu Leu Ser Asn Tyr Ser Tyr Leu Cys  
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Gln Pro Val Asp Tyr Ser Thr Ser Pro Leu Ala Met Arg Met Ala Lys  
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Val Cys Trp Trp Phe Phe Phe Ser Lys Val Ile Glu Leu Ala Asp Thr  
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Val Phe Phe Ile Leu Arg Lys Lys Asn Ser Gln Leu Thr Phe Leu His  
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Val Tyr His His Gly Thr Met Ile Phe Asn Trp Trp Ala Gly Val Lys  
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Tyr Leu Ala Gly Gly Gln Ser Phe Phe Ile Gly Leu Leu Asn Thr Phe  
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Val His Ile Val Met Tyr Ser Tyr Tyr Gly Leu Ala Ala Leu Gly Pro  
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His Thr Gln Lys Tyr Leu Trp Trp Lys Arg Tyr Leu Thr Ser Leu Gln  
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Leu Leu Gln Phe Val Leu Leu Thr Thr His Thr Gly Tyr Asn Leu Phe  
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Thr Glu Cys Asp Phe Pro Asp Ser Met Asn Ala Val Val Phe Ala Tyr  
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Met Cys Ser Ser Pro Pro Ser Gln Ser Lys Thr Thr Ser Leu Leu Ala	
1 5 10 15	
cgg tac acc acc gcc gcc ctc ctc ctc ctc acc ctc aca aca tgg tgc	96
Arg Tyr Thr Thr Ala Ala Leu Leu Leu Leu Thr Leu Thr Thr Trp Cys	
20 25 30	
cac ttc gcc ttc cca gcc gcc acc gcc aca ccc ggc ctc acc gcc gaa	144
His Phe Ala Phe Pro Ala Ala Thr Ala Thr Pro Gly Leu Thr Ala Glu	
35 40 45	
atg cac tcc tac aaa gtc cca ctc ggt ctc acc gta ttc tac ctg ctg	192
Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu	
50 55 60	
agt cta ccg tca cta aag tac gtt acg gac aac tac ctt gcc aaa aag	240
Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys	
65 70 75 80	
tat gat atg aag tca ctc cta acg gaa tca atg gtg ttg tac aat gtg	288
Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val	
85 90 95	
gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg	336
Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala	
100 105 110	
gtg atg aat aga gac cat ccg ttt att gga agt aga agt ttg gtt ggg	384
Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly	
115 120 125	
gcg gcg ttg cat agt ggg agc tcg tat gcg gtg tgg gtt cat tat tgt	432
Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys	
130 135 140	
gat aag tat ttg gag ttc ttt gat acg tat ttt atg gtg ttg agg ggg	480
Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly	
145 150 155 160	
aaa atg gac cag gtc tcc ttc ctc cac atc tac cac cac acg acc ata	528
Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile	
165 170 175	
gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggt gga gac att	576
Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile	
180 185 190	
tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc atg tat tcc	624
Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser	
195 200 205	
tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg aaa cga tac	672
Tyr Tyr Ala Leu Ala Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr	
210 215 220	
ctg act caa gct caa tta ttg caa ttc aca agt gtg gtg gtt tat acg	720
Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr	
225 230 235 240	
ggg tgt acg ggt tat act cat tac tat cat acg aag cat gga gcg gat	768
Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp	

245	250	255	
gag aca cag cct agt tta gga acg tat tat ttc tgt tgt gga gtg cag			816
Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln			
260	265	270	
gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc ttt tat aaa			864
Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys			
275	280	285	
cga tcc tat tct aag aag aac aag tca gga gga aag gat agc aag aag			912
Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys			
290	295	300	
aat gat gat ggg aat aat gag gat caa tgt cac aag gct atg aag gat			960
Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp			
305	310	315	320
ata tct gag ggt gcg aag gag gtt gtg ggg cat gca gcg aag gat gct			1008
Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala			
325	330	335	
gga aag ttg gtg gct acg gcg agt aag gct gta aag agg aag gga act			1056
Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr			
340	345	350	
cgt gtt act ggt gcc atg tag			1077
Arg Val Thr Gly Ala Met			
355			
<210> 60			
<211> 358			
<212> PRT			
<213> Thalassiosira pseudonana			
<400> 60			
Met Cys Ser Ser Pro Pro Ser Gln Ser Lys Thr Thr Ser Leu Leu Ala			
1	5	10	15
Arg Tyr Thr Thr Ala Ala Leu Leu Leu Leu Thr Leu Thr Thr Trp Cys			
20	25	30	
His Phe Ala Phe Pro Ala Ala Thr Ala Thr Pro Gly Leu Thr Ala Glu			
35	40	45	
Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu			
50	55	60	
Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys			
65	70	75	80
Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val			
85	90	95	
Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala			
100	105	110	
Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly			
115	120	125	

Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys  
 130 135 140

Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly  
 145 150 155 160

Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile  
 165 170 175

Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile  
 180 185 190

Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser  
 195 200 205

Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr  
 210 215 220

Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr  
 225 230 235 240

Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp  
 245 250 255

Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln  
 260 265 270

Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys  
 275 280 285

Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys  
 290 295 300

Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp  
 305 310 315 320

Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala  
 325 330 335

Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr  
 340 345 350

Arg Val Thr Gly Ala Met  
 355

<210> 61

<211> 933

<212> DNA

<213> *Thalassiosira pseudonana*

<220>

<221> CDS  
 <222> (1)..(933)  
 <223> Delta-5-Elongase

<400> 61  
 atg cac tcc tac aaa gtc cca ctc ggt ctc acc gta ttc tac ctg ctg 48  
 Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu  
 1 5 10 15  
 agt cta ccg tca cta aag tac gtt acg gac aac tac ctt gcc aaa aag 96  
 Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys  
 20 25 30  
 tat gat atg aag tca ctc cta acg gaa tca atg gtg ttg tac aat gtg 144  
 Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val  
 35 40 45  
 gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg 192  
 Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala  
 50 55 60  
 gtg atg aat aga gac cat ccg ttt att gga agt aga agt ttg gtt ggg 240  
 Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly  
 65 70 75 80  
 gcg gcg ttg cat agt ggg agc tcg tat gcg gtg tgg gtt cat tat tgt 288  
 Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys  
 85 90 95  
 gat aag tat ttg gag ttc ttt gat acg tat ttt atg gtg ttg agg ggg 336  
 Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly  
 100 105 110  
 aaa atg gac cag gtc tcc ttc ctc cac atc tac cac cac acg acc ata 384  
 Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile  
 115 120 125  
 gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggt gga gac att 432  
 Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile  
 130 135 140  
 tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc atg tat tcc 480  
 Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser  
 145 150 155 160  
 tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg aaa cga tac 528  
 Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr  
 165 170 175  
 ctg act caa gct caa tta ttg caa ttc aca agt gtg gtg gtt tat acg 576  
 Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr  
 180 185 190  
 ggg tgt acg ggt tat act cat tac tat cat acg aag cat gga gcg gat 624  
 Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp  
 195 200 205  
 gag aca cag cct agt tta gga acg tat tat ttc tgt tgt gga gtg cag 672  
 Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln  
 210 215 220  
 gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc ttt tat aaa 720  
 Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys  
 225 230 235 240  
 cga tcc tat tcg aag aag aac aag tca gga gga aag gat agc aag aag 768  
 Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys

## 102

245	250	255	
aat gat gat ggg aat aat gag gat	caa tgt cac aag gct atg aag gat		816
Asn Asp Asp Gly Asn Asn Glu Asp	Gln Cys His Lys Ala Met Lys Asp		
260	265	270	
ata tcg gag ggt gcg aag gag gtt	gtg ggg cat gca gcg aag gat gct		864
Ile Ser Glu Gly Ala Lys Glu Val	Val Gly His Ala Ala Lys Asp Ala		
275	280	285	
gga aag ttg gtg gct acg gcg agt aag gct gta aag agg aag gga act			912
Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr			
290	295	300	
cgt gtt act ggt gcc atg tag			933
Arg Val Thr Gly Ala Met			
305	310		
<210>	62		
<211>	310		
<212>	PRT		
<213>	Thalassiosira pseudonana		
<400>	62		
Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu			
1	5	10	15
Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys			
20	25	30	
Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val			
35	40	45	
Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala			
50	55	60	
Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly			
65	70	75	80
Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys			
85	90	95	
Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly			
100	105	110	
Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile			
115	120	125	
Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile			
130	135	140	
Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser			
145	150	155	160
Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr			
165	170	175	

Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr  
 180 185 190

Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp  
 195 200 205

Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln  
 210 215 220

Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys  
 225 230 235 240

Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys  
 245 250 255

Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp  
 260 265 270

Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala  
 275 280 285

Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr  
 290 295 300

Arg Val Thr Gly Ala Met  
 305 310

<210> 63  
 <211> 933  
 <212> DNA  
 <213> Thalassiosira pseudonana

<220>  
 <221> CDS  
 <222> (1)..(933)  
 <223> Delta-5-Elongase

<400> 63  
 atg cac tcc tac aaa gtc cca ctc ggt ctc acc gta ttc tac ctg ctg 48  
 Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu  
 1 5 10 15

agt cta ccg tca cta aag tac gtt acg gac aac tac ctt gcc aaa aag 96  
 Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys  
 20 25 30

tat gat atg aag tca ctc cta acg gaa tca atg gtg ttg tac aat gtg 144  
 Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val  
 35 40 45

gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg 192  
 Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala  
 50 55 60

gtg atg aat aga gac cat ccg ttt att gga agt aga agt ttg gtt ggg 240  
 Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly

104

65	70	75	80	
gcg gcg ttg cat agt ggg agc tcg tat gcg gtg tgg gtt cat tat tgt				288
Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys				
	85	90	95	
gat aag tat ttg gag ttc ttt gat acg tat ttt atg gtg ttg agg ggg				336
Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly				
	100	105	110	
aaa atg gac cag gtc tcc ttc ctc cac atc tac cac cac acg acc ata				384
Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile				
	115	120	125	
gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggt gga gac att				432
Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile				
	130	135	140	
tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc atg tat tcc				480
Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser				
	145	150	155	160
tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg aaa cga tac				528
Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr				
	165	170	175	
ctg act caa gct caa tta ttg caa ttc aca agt gtg gtg gtt tat acg				576
Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr				
	180	185	190	
ggg tgt acg ggt tat act cat tac tat cat acg aag cat gga gcg gat				624
Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp				
	195	200	205	
gag aca cag cct agt tta gga acg tat tat ttc tgt tgt gga gtg cag				672
Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln				
	210	215	220	
gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc ttt tat aaa				720
Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys				
	225	230	235	240
cga tcc tat tcg aag aag aac aag tca gga gga aag gat agc aag aag				768
Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys				
	245	250	255	
aat gat gat ggg aat aat gag gat caa tgt cac aag gct atg aag gat				816
Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp				
	260	265	270	
ata tcg gag ggt gcg aag gag gtt gtg ggg cat gca gcg aag gat gct				864
Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala				
	275	280	285	
gga aag ttg gtg gct acg gcg agt aag gct gta aag agg aag gga act				912
Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr				
	290	295	300	
cgt gtt act ggt gcc atg tag				933
Arg Val Thr Gly Ala Met				
	305	310		
<210> 64				
<211> 310				
<212> PRT				
<213> Thalassiosira pseudonana				



&lt;400&gt; 64

Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu  
 1 5 10 15

Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys  
 20 25 30

Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val  
 35 40 45

Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala  
 50 55 60

Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly  
 65 70 75 80

Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys  
 85 90 95

Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly  
 100 105 110

Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile  
 115 120 125

Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile  
 130 135 140

Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser  
 145 150 155 160

Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr  
 165 170 175

Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr  
 180 185 190

Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp  
 195 200 205

Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln  
 210 215 220

Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys  
 225 230 235 240

Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys  
 245 250 255

Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp  
 260 265 270

Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala  
275 280 285

Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr  
290 295 300

Arg Val Thr Gly Ala Met  
305 310

<210> 65  
<211> 825  
<212> DNA  
<213> *Thraustochytrium aureum*

<220>  
<221> CDS  
<222> (1)..(825)  
<223> Delta-5-Elongase

<400> 65  
atg acg agc aac atg agc gcg tgg ggc gtc gcc gtc gac cag acg cag 48  
Met Thr Ser Asn Met Ser Ala Trp Gly Val Ala Val Asp Gln Thr Gln  
1 5 10 15  
cag gtc gtc gac cag atc atg ggc ggc gcc gag ccg tac aag ctg aca 96  
Gln Val Val Asp Gln Ile Met Gly Gly Ala Glu Pro Tyr Lys Leu Thr  
20 25 30  
gaa ggg cgc atg acg aac gtc gag acg atg ctg gcg atc gag tgc ggc 144  
Glu Gly Arg Met Thr Asn Val Glu Thr Met Leu Ala Ile Glu Cys Gly  
35 40 45  
tac gcc gcc atg ctg ctg ttc ctg acc ccg atc atg aag cag gcc gag 192  
Tyr Ala Ala Met Leu Leu Phe Leu Thr Pro Ile Met Lys Gln Ala Glu  
50 55 60  
aag ccc ttc gag ctc aag tcc ttc aag ctc gcc cac aac ctg ttc ctg 240  
Lys Pro Phe Glu Leu Lys Ser Phe Lys Leu Ala His Asn Leu Phe Leu  
65 70 75 80  
ttc gtc ctg tcc gcc tac atg tgc ctc gag acc gtc cgc cag gcc tac 288  
Phe Val Leu Ser Ala Tyr Met Cys Leu Glu Thr Val Arg Gln Ala Tyr  
85 90 95  
ctt gcg ggc tac tcg gtg ttc ggc aac gac atg gag aag ggc agc gag 336  
Leu Ala Gly Tyr Ser Val Phe Gly Asn Asp Met Glu Lys Gly Ser Glu  
100 105 110  
ccg cac gcg cac ggc atg gcc caa atc gtg tgg atc ttt tac gtg tcc 384  
Pro His Ala His Gly Met Ala Gln Ile Val Trp Ile Phe Tyr Val Ser  
115 120 125  
aag gcg tac gag ttc gtg gac acg ctg atc atg atc ctg tgc aaa aag 432  
Lys Ala Tyr Glu Phe Val Asp Thr Leu Ile Met Ile Leu Cys Lys Lys  
130 135 140  
ttc aac cag gtc tcc gtc ctg cac gtg tac cac cac gcc acc atc ttt 480  
Phe Asn Gln Val Ser Val Leu His Val Tyr His His Ala Thr Ile Phe  
145 150 155 160  
gct atc tgg ttt atg atc gcc aag tac gcc ccg ggc ggc gac gca tac 528  
Ala Ile Trp Phe Met Ile Ala Lys Tyr Ala Pro Gly Gly Asp Ala Tyr

## 107

165	170	175	
ttt agc gtc atc ctg aac tcg ttc gtg cac acc gtc atg tac gcg tac			576
Phe Ser Val Ile Leu Asn Ser Phe Val His Thr Val Met Tyr Ala Tyr			
180	185	190	
tac ttc ttc tcg tcg cag ggc ttc ggg ttc gtc aag ccg atc aag ccg			624
Tyr Phe Phe Ser Ser Gln Gly Phe Gly Phe Val Lys Pro Ile Lys Pro			
195	200	205	
tac atc acc tcg ctg cag atg acg cag ttc atg gcg atg ctc gtg cag			672
Tyr Ile Thr Ser Leu Gln Met Thr Gln Phe Met Ala Met Leu Val Gln			
210	215	220	
tcg ctg tac gac tac ctt tac ccg tgc gac tac ccg cag ggg ctc gtc			720
Ser Leu Tyr Asp Tyr Leu Tyr Pro Cys Asp Tyr Pro Gln Gly Leu Val			
225	230	235	240
aag ctc ctc ggc gtg tac atg ctc acc ctg ctt gcg ctc ttc ggc aac			768
Lys Leu Leu Gly Val Tyr Met Leu Thr Leu Leu Ala Leu Phe Gly Asn			
245	250	255	
ttt ttc gtg cag agc tac ctc aag aag tcg aac aag ccc aag gcc aag			816
Phe Phe Val Gln Ser Tyr Leu Lys Lys Ser Asn Lys Pro Lys Ala Lys			
260	265	270	
tcg gcc taa			825
Ser Ala			

<210> 66  
 <211> 274  
 <212> PRT  
 <213> *Thraustochytrium aureum*

<400> 66

Met Thr Ser Asn Met Ser Ala Trp Gly Val Ala Val Asp Gln Thr Gln			
1	5	10	15

Gln Val Val Asp Gln Ile Met Gly Gly Ala Glu Pro Tyr Lys Leu Thr			
20	25	30	

Glu Gly Arg Met Thr Asn Val Glu Thr Met Leu Ala Ile Glu Cys Gly			
35	40	45	

Tyr Ala Ala Met Leu Leu Phe Leu Thr Pro Ile Met Lys Gln Ala Glu			
50	55	60	

Lys Pro Phe Glu Leu Lys Ser Phe Lys Leu Ala His Asn Leu Phe Leu			
65	70	75	80

Phe Val Leu Ser Ala Tyr Met Cys Leu Glu Thr Val Arg Gln Ala Tyr			
85	90	95	

Leu Ala Gly Tyr Ser Val Phe Gly Asn Asp Met Glu Lys Gly Ser Glu			
100	105	110	

Pro His Ala His Gly Met Ala Gln Ile Val Trp Ile Phe Tyr Val Ser			
115	120	125	

Lys Ala Tyr Glu Phe Val Asp Thr Leu Ile Met Ile Leu Cys Lys Lys  
 130 135 140

Phe Asn Gln Val Ser Val Leu His Val Tyr His His Ala Thr Ile Phe  
 145 150 155 160

Ala Ile Trp Phe Met Ile Ala Lys Tyr Ala Pro Gly Gly Asp Ala Tyr  
 165 170 175

Phe Ser Val Ile Leu Asn Ser Phe Val His Thr Val Met Tyr Ala Tyr  
 180 185 190

Tyr Phe Phe Ser Ser Gln Gly Phe Gly Phe Val Lys Pro Ile Lys Pro  
 195 200 205

Tyr Ile Thr Ser Leu Gln Met Thr Gln Phe Met Ala Met Leu Val Gln  
 210 215 220

Ser Leu Tyr Asp Tyr Leu Tyr Pro Cys Asp Tyr Pro Gln Gly Leu Val  
 225 230 235 240

Lys Leu Leu Gly Val Tyr Met Leu Thr Leu Leu Ala Leu Phe Gly Asn  
 245 250 255

Phe Phe Val Gln Ser Tyr Leu Lys Lys Ser Asn Lys Pro Lys Ala Lys  
 260 265 270

Ser Ala

<210> 67  
 <211> 903  
 <212> DNA  
 <213> *Ostreococcus tauri*

<220>  
 <221> CDS  
 <222> (1)..(903)  
 <223> Delta-5-Elongase

<400> 67  
 atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg ttc gcc gcg tac 48  
 Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr  
 1 5 10 15

gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc 96  
 Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly  
 20 25 30

atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg 144  
 Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg  
 35 40 45

ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga 192  
 Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly

50	55	60	
ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg			240
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met			
65	70	75	80
ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg			288
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly			
	85	90	95
atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca			336
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser			
	100	105	110
acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg			384
Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val			
	115	120	125
tgg ttg cac tac aac aac caa tat ttg gag cta ttg gac act gtg ttc			432
Trp Leu His Tyr Asn Asn Gln Tyr Leu Glu Leu Leu Asp Thr Val Phe			
	130	135	140
atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat			480
Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr			
	145	150	155
cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg			528
His His Ala Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met			
	165	170	175
gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg			576
Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser			
	180	185	190
ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc			624
Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly			
	195	200	205
att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa			672
Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln			
	210	215	220
ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac			720
Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His			
	225	230	235
tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg			768
Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met			
	245	250	255
ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg			816
Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser			
	260	265	270
cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg			864
Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala			
	275	280	285
ccc agc gtg cga cgc acg cga tct cga aaa att gac taa			903
Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp			
	290	295	300

&lt;210&gt; 68

&lt;211&gt; 300

&lt;212&gt; PRT

<213> *Ostreococcus tauri*

&lt;400&gt; 68

Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr  
1 5 10 15

Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly  
20 25 30

Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg  
35 40 45

Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly  
50 55 60

Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met  
65 70 75 80

Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly  
85 90 95

Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser  
100 105 110

Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val  
115 120 125

Trp Leu His Tyr Asn Asn Gln Tyr Leu Glu Leu Leu Asp Thr Val Phe  
130 135 140

Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr  
145 150 155 160

His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met  
165 170 175

Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser  
180 185 190

Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly  
195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln  
210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His  
225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met  
245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser  
260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala  
 275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp  
 290 295 300

<210> 69  
 <211> 879  
 <212> DNA  
 <213> *Ostreococcus tauri*

<220>  
 <221> CDS  
 <222> (1)..(879)  
 <223> Delta-6-Elongase

<400> 69  
 atg agt ggc tta cgt gca ccc aac ttt tta cac aga ttc tgg aca aag 48  
 Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys  
 1 5 10 15  
 tgg gac tac gcg att tcc aaa gtc gtc ttc acg tgt gcc gac agt ttt 96  
 Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe  
 20 25 30  
 cag tgg gac atc ggg cca gtg agt tgc agt acg gcg cat tta ccc gcc 144  
 Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala  
 35 40 45  
 att gaa tcc cct acc cca ctg gtg act agc ctc ttg ttc tac tta gtc 192  
 Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val  
 50 55 60  
 aca gtt ttc ttg tgg tat ggt cgt tta acc agg agt tca gac aag aaa 240  
 Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys  
 65 70 75 80  
 att aga gag cct acg tgg tta aga aga ttc ata ata tgt cat aat gcg 288  
 Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala  
 85 90 95  
 ttc ttg ata gtc ctc agt ctt tac atg tgc ctt ggt tgt gtg gcc caa 336  
 Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln  
 100 105 110  
 gcg tat cag aat gga tat act tta tgg ggt aat gaa ttc aag gcc acg 384  
 Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr  
 115 120 125  
 gaa act cag ctt gct ctc tac att tac att ttt tac gta agt aaa ata 432  
 Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile  
 130 135 140  
 tac gag ttt gta gat act tac att atg ctt ctc aag aat aac ttg cgg 480  
 Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg  
 145 150 155 160  
 caa gta agt ttc cta cac att tat cac cac agc acg att tcc ttt att 528  
 Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile  
 165 170 175  
 tgg tgg atc att gct cgg agg gct ccg ggt ggt gat gct tac ttc agc 576  
 Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser

180	185	190	
gcg gcc ttg aac tca tgg gta cac gtg tgc atg tac acc tat tat cta Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu 195 200 205			624
tta tca acc ctt att gga aaa gaa gat cct aag cgt tcc aac tac ctt Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu 210 215 220			672
tgg tgg ggt cgc cac cta acg caa atg cag atg ctt cag ttt ttc ttc Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe 225 230 235 240			720
aac gta ctt caa gcg ttg tac tgc gct tcg ttc tct acg tat ccc aag Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys 245 250 255			768
ttt ttg tcc aaa att ctg ctc gtc tat atg atg agc ctt ctc ggc ttg Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu 260 265 270			816
ttt ggg cat ttc tac tat tcc aag cac ata gca gca gct aag ctc cag Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln 275 280 285			864
aaa aaa cag cag tga Lys Lys Gln Gln 290			879

<210> 70  
 <211> 292  
 <212> PRT  
 <213> *Ostreococcus tauri*  
 <400> 70

Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys  
 1 5 10 15

Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe  
 20 25 30

Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala  
 35 40 45

Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val  
 50 55 60

Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys  
 65 70 75 80

Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala  
 85 90 95

Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln  
 100 105 110

Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr  
 115 120 125



Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile  
 130 135 140

Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg  
 145 150 155 160

Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile  
 165 170 175

Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser  
 180 185 190

Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu  
 195 200 205

Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu  
 210 215 220

Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe  
 225 230 235 240

Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys  
 245 250 255

Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu  
 260 265 270

Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln  
 275 280 285

Lys Lys Gln Gln  
 290

<210> 71  
 <211> 1362  
 <212> DNA  
 <213> *Primula farinosa*

<220>  
 <221> CDS  
 <222> (1)..(1362)  
 <223> Delta-6-Desaturase

<400> 71  
 atg gct aac aaa tct cca cca aac ccc aaa aca ggt tac ata acc agc 48  
 Met Ala Asn Lys Ser Pro Pro Asn Pro Lys Thr Gly Tyr Ile Thr Ser  
 1 5 10 15

tca gac ctg aaa tcc cac aac aag gca ggt gac cta tgg ata tca atc 96  
 Ser Asp Leu Lys Ser His Asn Lys Ala Gly Asp Leu Trp Ile Ser Ile  
 20 25 30

cac ggc caa gtc tac gac gtg tcc tct tgg gcc gcc ctt cat ccg ggg 144  
 His Gly Gln Val Tyr Asp Val Ser Ser Trp Ala Ala Leu His Pro Gly

35	40	45	
ggc act gcc cct ctc atg gcc ctt gca gga cac gac gtg acc gat gct Gly Thr Ala Pro Leu Met Ala Leu Ala Gly His Asp Val Thr Asp Ala 50 55 60			192
ttc ctc gcg tac cat ccc cct tcc act gcc cgt ctc ctc cct cct ctc Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu 65 70 75 80			240
tct acc aac ctc ctt ctt caa aac cac tcc gtc tcc ccc acc tcc tca Ser Thr Asn Leu Leu Leu Gln Asn His Ser Val Ser Pro Thr Ser Ser 85 90 95			288
gac tac cgc aaa ctc ctc gac aac ttc cat aaa cat ggc ctt ttc cgc Asp Tyr Arg Lys Leu Leu Asp Asn Phe His Lys His Gly Leu Phe Arg 100 105 110			336
gcc agg gcc cac act gct tac gcc acc ttc gtc ttc atg ata gcg atg Ala Arg Gly His Thr Ala Tyr Ala Thr Phe Val Phe Met Ile Ala Met 115 120 125			384
ttt cta atg agc gtg act gga gtc ctt tgc agc gac agt gcg tgg gtc Phe Leu Met Ser Val Thr Gly Val Leu Cys Ser Asp Ser Ala Trp Val 130 135 140			432
cat ttg gct agc gcc gga gca atg ggg ttc gcc tgg atc caa tgc gga His Leu Ala Ser Gly Gly Ala Met Gly Phe Ala Trp Ile Gln Cys Gly 145 150 155 160			480
tgg ata ggt cac gac tct ggg cat tac cgg att atg tct gac agg aaa Trp Ile Gly His Asp Ser Gly His Tyr Arg Ile Met Ser Asp Arg Lys 165 170 175			528
tgg aac tgg ttc gcg caa atc cta agc aca aac tgc ctc cag ggg att Trp Asn Trp Phe Ala Gln Ile Leu Ser Thr Asn Cys Leu Gln Gly Ile 180 185 190			576
agt atc ggg tgg tgg aag tgg aac cat aat gcg cac cac atc gct tgc Ser Ile Gly Trp Trp Lys Trp Asn His Asn Ala His His Ile Ala Cys 195 200 205			624
aat agc ctg gat tac gac ccc gac ctc cag tat atc cct ttg ctc gtc Asn Ser Leu Asp Tyr Asp Pro Asp Leu Gln Tyr Ile Pro Leu Leu Val 210 215 220			672
gtc tcc ccc aag ttc ttc aac tcc ctt act tct cgt ttc tac gac aag Val Ser Pro Lys Phe Phe Asn Ser Leu Thr Ser Arg Phe Tyr Asp Lys 225 230 235 240			720
aag ctg aac ttc gac gcc gtg tgg agg ttt ctg gtt tgc tac cag cac Lys Leu Asn Phe Asp Gly Val Ser Arg Phe Leu Val Cys Tyr Gln His 245 250 255			768
tgg acg ttt tat ccg gtc atg tgt gtc gct agg ctg aac atg ctc gcg Trp Thr Phe Tyr Pro Val Met Cys Val Ala Arg Leu Asn Met Leu Ala 260 265 270			816
cag tca ttt ata acg ctt ttc tgg agt agg gag gtg tgc cat agg gcg Gln Ser Phe Ile Thr Leu Phe Ser Ser Arg Glu Val Cys His Arg Ala 275 280 285			864
caa gag gtt ttc gga ctt gcc gtg ttt tgg gtt tgg ttt ccg ctt tta Gln Glu Val Phe Gly Leu Ala Val Phe Trp Val Phe Pro Leu Leu 290 295 300			912
ctt tct tgt tta cct aat tgg gcc gag agg att atg ttt ttg ctt gcg Leu Ser Cys Leu Pro Asn Trp Gly Glu Arg Ile Met Phe Leu Leu Ala 305 310 315 320			960

## 115

305                      310                      315                      320  
 agc tat tcc gtt acg ggg ata caa cac gtg cag ttc agc ttg aac cat      1008  
 Ser Tyr Ser Val Thr Gly Ile Gln His Val Gln Phe Ser Leu Asn His  
                          325                      330                      335  
 ttt tct tcg gac gtc tat gtg ggc ccg cca gta ggt aat gac tgg ttc      1056  
 Phe Ser Ser Asp Val Tyr Val Gly Pro Pro Val Gly Asn Asp Trp Phe  
                          340                      345                      350  
 aag aaa cag act gcc ggg aca ctt aac ata tcg tgc ccg gcg tgg atg      1104  
 Lys Lys Gln Thr Ala Gly Thr Leu Asn Ile Ser Cys Pro Ala Trp Met  
                          355                      360                      365  
 gat tgg ttc cat ggc ggg tta cag ttt cag gtc gag cac cac ttg ttt      1152  
 Asp Trp Phe His Gly Gly Leu Gln Phe Gln Val Glu His His Leu Phe  
                          370                      375                      380  
 ccg cgg atg cct agg ggt cag ttt agg aag att tct cct ttt gtg agg      1200  
 Pro Arg Met Pro Arg Gly Gln Phe Arg Lys Ile Ser Pro Phe Val Arg  
                          385                      390                      395                      400  
 gat ttg tgt aag aaa cac aac ttg cct tac aat atc gcg tct ttt act      1248  
 Asp Leu Cys Lys Lys His Asn Leu Pro Tyr Asn Ile Ala Ser Phe Thr  
                          405                      410                      415  
 aaa gcg aat gtg ttt acg ctt aag acg ctg aga aat acg gcc att gag      1296  
 Lys Ala Asn Val Phe Thr Leu Lys Thr Leu Arg Asn Thr Ala Ile Glu  
                          420                      425                      430  
 gct cgg gac ctc tct aat ccg ctc cca aag aat atg gtg tgg gaa gct      1344  
 Ala Arg Asp Leu Ser Asn Pro Leu Pro Lys Asn Met Val Trp Glu Ala  
                          435                      440                      445  
 ctt aaa act ctc ggg tga      1362  
 Leu Lys Thr Leu Gly  
                          450

<210> 72  
 <211> 453  
 <212> PRT  
 <213> *Primula farinosa*

<400> 72

Met Ala Asn Lys Ser Pro Pro Asn Pro Lys Thr Gly Tyr Ile Thr Ser  
 1                      5                      10                      15

Ser Asp Leu Lys Ser His Asn Lys Ala Gly Asp Leu Trp Ile Ser Ile  
                          20                      25                      30

His Gly Gln Val Tyr Asp Val Ser Ser Trp Ala Ala Leu His Pro Gly  
                          35                      40                      45

Gly Thr Ala Pro Leu Met Ala Leu Ala Gly His Asp Val Thr Asp Ala  
                          50                      55                      60

Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu  
 65                      70                      75                      80

Ser Thr Asn Leu Leu Leu Gln Asn His Ser Val Ser Pro Thr Ser Ser  
                          85                      90                      95

Asp Tyr Arg Lys Leu Leu Asp Asn Phe His Lys His Gly Leu Phe Arg  
 100 105 110

Ala Arg Gly His Thr Ala Tyr Ala Thr Phe Val Phe Met Ile Ala Met  
 115 120 125

Phe Leu Met Ser Val Thr Gly Val Leu Cys Ser Asp Ser Ala Trp Val  
 130 135 140

His Leu Ala Ser Gly Gly Ala Met Gly Phe Ala Trp Ile Gln Cys Gly  
 145 150 155 160

Trp Ile Gly His Asp Ser Gly His Tyr Arg Ile Met Ser Asp Arg Lys  
 165 170 175

Trp Asn Trp Phe Ala Gln Ile Leu Ser Thr Asn Cys Leu Gln Gly Ile  
 180 185 190

Ser Ile Gly Trp Trp Lys Trp Asn His Asn Ala His His Ile Ala Cys  
 195 200 205

Asn Ser Leu Asp Tyr Asp Pro Asp Leu Gln Tyr Ile Pro Leu Leu Val  
 210 215 220

Val Ser Pro Lys Phe Phe Asn Ser Leu Thr Ser Arg Phe Tyr Asp Lys  
 225 230 235 240

Lys Leu Asn Phe Asp Gly Val Ser Arg Phe Leu Val Cys Tyr Gln His  
 245 250 255

Trp Thr Phe Tyr Pro Val Met Cys Val Ala Arg Leu Asn Met Leu Ala  
 260 265 270

Gln Ser Phe Ile Thr Leu Phe Ser Ser Arg Glu Val Cys His Arg Ala  
 275 280 285

Gln Glu Val Phe Gly Leu Ala Val Phe Trp Val Trp Phe Pro Leu Leu  
 290 295 300

Leu Ser Cys Leu Pro Asn Trp Gly Glu Arg Ile Met Phe Leu Leu Ala  
 305 310 315 320

Ser Tyr Ser Val Thr Gly Ile Gln His Val Gln Phe Ser Leu Asn His  
 325 330 335

Phe Ser Ser Asp Val Tyr Val Gly Pro Pro Val Gly Asn Asp Trp Phe  
 340 345 350

Lys Lys Gln Thr Ala Gly Thr Leu Asn Ile Ser Cys Pro Ala Trp Met  
 355 360 365

Asp Trp Phe His Gly Gly Leu Gln Phe Gln Val Glu His His Leu Phe  
370 375 380

Pro Arg Met Pro Arg Gly Gln Phe Arg Lys Ile Ser Pro Phe Val Arg  
385 390 395 400

Asp Leu Cys Lys Lys His Asn Leu Pro Tyr Asn Ile Ala Ser Phe Thr  
405 410 415

Lys Ala Asn Val Phe Thr Leu Lys Thr Leu Arg Asn Thr Ala Ile Glu  
420 425 430

Ala Arg Asp Leu Ser Asn Pro Leu Pro Lys Asn Met Val Trp Glu Ala  
435 440 445

Leu Lys Thr Leu Gly  
450

<210> 73  
<211> 1362  
<212> DNA  
<213> *Primula vialii*

<220>  
<221> CDS  
<222> (1)..(1362)  
<223> Delta-6-Desaturase

<400> 73  
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Met Ala Asn Lys Ser Pro Pro Asn Pro Lys Thr Gly Tyr Ile Thr Ser  
1 5 10 15  
tca gac ctg aaa ggg cac aac aaa gca gga gac cta tgg ata tca atc 96  
Ser Asp Leu Lys Gly His Asn Lys Ala Gly Asp Leu Trp Ile Ser Ile  
20 25 30  
cac ggg gag gta tac gac gtg tcc tcg tgg gcc ggc ctt cac ccg ggg 144  
His Gly Glu Val Tyr Asp Val Ser Ser Trp Ala Gly Leu His Pro Gly  
35 40 45  
ggc agt gcc ccc ctc atg gcc ctc gca gga cac gac gta acc gac gct 192  
Gly Ser Ala Pro Leu Met Ala Leu Ala Gly His Asp Val Thr Asp Ala  
50 55 60  
ttt cta gcg tat cat cct cct tct acc gcc cgc ctc ctc cct ccc ctc 240  
Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu  
65 70 75 80  
tcc acc aac ctc ctc ctt caa aac cac tcc gtc tcc ccc acc tcc tct 288  
Ser Thr Asn Leu Leu Leu Gln Asn His Ser Val Ser Pro Thr Ser Ser  
85 90 95  
gac tac cgc aaa ctc ctc cac aac ttc cat aaa att ggt atg ttc cgc 336  
Asp Tyr Arg Lys Leu Leu His Asn Phe His Lys Ile Gly Met Phe Arg  
100 105 110  
gcc agg ggc cac act gct tac gcc acc ttc gtc atc atg ata gtg atg 384  
Ala Arg Gly His Thr Ala Tyr Ala Thr Phe Val Ile Met Ile Val Met

115	120	125	
ttt cta acg agc gtg acc gga gtc ctt tgc agc gac agt gcg tgg gtc Phe Leu Thr Ser Val Thr Gly Val Leu Cys Ser Asp Ser Ala Trp Val 130 135 140			432
cat ctg gct agc ggc gca gca atg ggg ttc gcc tgg atc cag tgc gga His Leu Ala Ser Gly Ala Ala Met Gly Phe Ala Trp Ile Gln Cys Gly 145 150 155 160			480
tgg ata ggt cac gac tct ggg cat tac cgg att atg tct gac agg aaa Trp Ile Gly His Asp Ser Gly His Tyr Arg Ile Met Ser Asp Arg Lys 165 170 175			528
tgg aac tgg ttc gcg cag gtc ctg agc aca aac tgc ctc cag ggg atc Trp Asn Trp Phe Ala Gln Val Leu Ser Thr Asn Cys Leu Gln Gly Ile 180 185 190			576
agt atc ggg tgg tgg aag tgg aac cat aac gcc cac cac att gct tgc Ser Ile Gly Trp Trp Lys Trp Asn His Asn Ala His Ile Ala Cys 195 200 205			624
aat agc ctg gac tac gac ccc gac ctc cag tat atc cct ttg ctc gtg Asn Ser Leu Asp Tyr Asp Pro Asp Leu Gln Tyr Ile Pro Leu Leu Val 210 215 220			672
gtc tcc ccc aag ttc ttc aac tcc ctt act tct cgt ttc tac gac aag Val Ser Pro Lys Phe Phe Asn Ser Leu Thr Ser Arg Phe Tyr Asp Lys 225 230 235 240			720
aag ctg aat ttc gac ggc gtg tca agg ttt ctg gtt tgc tac cag cac Lys Leu Asn Phe Asp Gly Val Ser Arg Phe Leu Val Cys Tyr Gln His 245 250 255			768
tgg acg ttt tat cca gtc atg tgt gtc gct agg cta aac atg atc gca Trp Thr Phe Tyr Pro Val Met Cys Val Ala Arg Leu Asn Met Ile Ala 260 265 270			816
cag tcg ttt ata acg ctt ttc tcg agc agg gag gtg ggt cat agg gcg Gln Ser Phe Ile Thr Leu Phe Ser Ser Arg Glu Val Gly His Arg Ala 275 280 285			864
caa gag att ttc gga ctt gct gtg ttt tgg gtt tgg ttt ccg ctc ctg Gln Glu Ile Phe Gly Leu Ala Val Phe Trp Val Trp Phe Pro Leu Leu 290 295 300			912
ctc tct tgc tta cct aat tgg agc gag agg att atg ttt ctg cta gcg Leu Ser Cys Leu Pro Asn Trp Ser Glu Arg Ile Met Phe Leu Leu Ala 305 310 315 320			960
agc tat tcc gtt acg ggg ata cag cac gtg cag ttc agc ttg aac cat Ser Tyr Ser Val Thr Gly Ile Gln His Val Gln Phe Ser Leu Asn His 325 330 335			1008
ttt tct tcg gac gtc tac gtg ggc ccg cca gta gct aac gac tgg ttc Phe Ser Ser Asp Val Tyr Val Gly Pro Pro Val Ala Asn Asp Trp Phe 340 345 350			1056
aag aaa cag act gct ggg aca ctt aac ata tcg tgc ccg gcg tgg atg Lys Lys Gln Thr Ala Gly Thr Leu Asn Ile Ser Cys Pro Ala Trp Met 355 360 365			1104
gac tgg ttc cat ggc ggg ttg cag ttt cag gtc gag cac cac ttg ttt Asp Trp Phe His Gly Gly Leu Gln Phe Gln Val Glu His His Leu Phe 370 375 380			1152
ccg cgg atg cct agg ggt cag ttt agg aag att tct cct ttt gtg agg Pro Arg Met Pro Arg Gly Gln Phe Arg Lys Ile Ser Pro Phe Val Arg			1200

119

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385          390          395          400
gat ttg tgt aag aaa cac aac ttg cct tac aat atc gcg tct ttt act    1248
Asp Leu Cys Lys Lys His Asn Leu Pro Tyr Asn Ile Ala Ser Phe Thr.
          405          410          415

aaa gca aac gtg ttg acg ctt aag acg ctg aga aat acg gcc att gag    1296
Lys Ala Asn Val Leu Thr Leu Lys Thr Leu Arg Asn Thr Ala Ile Glu
          420          425          430

gct cgg gac ctc tct aat ccg acc cca aag aat atg gtg tgg gaa gcc    1344
Ala Arg Asp Leu Ser Asn Pro Thr Pro Lys Asn Met Val Trp Glu Ala
          435          440          445

gtc cac aca cac ggc tag    1362
Val His Thr His Gly
          450

<210> 74
<211> 453
<212> PRT
<213> Primula vialii

<400> 74

Met Ala Asn Lys Ser Pro Pro Asn Pro Lys Thr Gly Tyr Ile Thr Ser
1          5          10          15

Ser Asp Leu Lys Gly His Asn Lys Ala Gly Asp Leu Trp Ile Ser Ile
20          25          30

His Gly Glu Val Tyr Asp Val Ser Ser Trp Ala Gly Leu His Pro Gly
35          40          45

Gly Ser Ala Pro Leu Met Ala Leu Ala Gly His Asp Val Thr Asp Ala
50          55          60

Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu
65          70          75          80

Ser Thr Asn Leu Leu Leu Gln Asn His Ser Val Ser Pro Thr Ser Ser
85          90          95

Asp Tyr Arg Lys Leu Leu His Asn Phe His Lys Ile Gly Met Phe Arg
100          105          110

Ala Arg Gly His Thr Ala Tyr Ala Thr Phe Val Ile Met Ile Val Met
115          120          125

Phe Leu Thr Ser Val Thr Gly Val Leu Cys Ser Asp Ser Ala Trp Val
130          135          140

His Leu Ala Ser Gly Ala Ala Met Gly Phe Ala Trp Ile Gln Cys Gly
145          150          155          160

Trp Ile Gly His Asp Ser Gly His Tyr Arg Ile Met Ser Asp Arg Lys
165          170          175

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Trp Asn Trp Phe Ala Gln Val Leu Ser Thr Asn Cys Leu Gln Gly Ile  
 180 185 190

Ser Ile Gly Trp Trp Lys Trp Asn His Asn Ala His His Ile Ala Cys  
 195 200 205

Asn Ser Leu Asp Tyr Asp Pro Asp Leu Gln Tyr Ile Pro Leu Leu Val  
 210 215 220

Val Ser Pro Lys Phe Phe Asn Ser Leu Thr Ser Arg Phe Tyr Asp Lys  
 225 230 235 240

Lys Leu Asn Phe Asp Gly Val Ser Arg Phe Leu Val Cys Tyr Gln His  
 245 250 255

Trp Thr Phe Tyr Pro Val Met Cys Val Ala Arg Leu Asn Met Ile Ala  
 260 265 270

Gln Ser Phe Ile Thr Leu Phe Ser Ser Arg Glu Val Gly His Arg Ala  
 275 280 285

Gln Glu Ile Phe Gly Leu Ala Val Phe Trp Val Trp Phe Pro Leu Leu  
 290 295 300

Leu Ser Cys Leu Pro Asn Trp Ser Glu Arg Ile Met Phe Leu Leu Ala  
 305 310 315 320

Ser Tyr Ser Val Thr Gly Ile Gln His Val Gln Phe Ser Leu Asn His  
 325 330 335

Phe Ser Ser Asp Val Tyr Val Gly Pro Pro Val Ala Asn Asp Trp Phe  
 340 345 350

Lys Lys Gln Thr Ala Gly Thr Leu Asn Ile Ser Cys Pro Ala Trp Met  
 355 360 365

Asp Trp Phe His Gly Gly Leu Gln Phe Gln Val Glu His His Leu Phe  
 370 375 380

Pro Arg Met Pro Arg Gly Gln Phe Arg Lys Ile Ser Pro Phe Val Arg  
 385 390 395 400

Asp Leu Cys Lys Lys His Asn Leu Pro Tyr Asn Ile Ala Ser Phe Thr  
 405 410 415

Lys Ala Asn Val Leu Thr Leu Lys Thr Leu Arg Asn Thr Ala Ile Glu  
 420 425 430

Ala Arg Asp Leu Ser Asn Pro Thr Pro Lys Asn Met Val Trp Glu Ala  
 435 440 445



Val His Thr His Gly  
450

<210> 75  
<211> 903  
<212> DNA  
<213> *Ostreococcus tauri*

<220>  
<221> CDS  
<222> (1)..(903)  
<223> Delta-5-Elongase

<400> 75  
atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg tcc gcc gcg tac 48  
Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Ser Ala Ala Tyr  
1 5 10 15  
gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc 96  
Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly  
20 25 30  
atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg 144  
Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg  
35 40 45  
ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga 192  
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly  
50 55 60  
ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg 240  
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met  
65 70 75 80  
ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg 288  
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly  
85 90 95  
atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca 336  
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser  
100 105 110  
acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg 384  
Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val  
115 120 125  
tgg ttg cac tac aac aac aaa tat ttg gag cta ttg gac act gtg ttc 432  
Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe  
130 135 140  
atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat 480  
Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr  
145 150 155 160  
cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg 528  
His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met  
165 170 175  
gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg 576  
Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser  
180 185 190  
ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc 624  
Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly

195	200	205	
att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa			672
Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln			
210	215	220	
ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac			720
Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His			
225	230	235	240
tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg			768
Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met			
	245	250	255
ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg			816
Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser			
	260	265	270
cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg			864
Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala			
	275	280	285
ccc agc gtg cga cgc acg cga tct cga aaa att gac taa			903
Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp			
	290	295	300
<210> 76			
<211> 300			
<212> PRT			
<213> Ostreococcus tauri			
<400> 76			
Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Ser Ala Ala Tyr			
1	5	10	15
Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly			
	20	25	30
Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg			
	35	40	45
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly			
	50	55	60
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met			
	65	70	75
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly			
	85	90	95
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser			
	100	105	110
Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val			
	115	120	125
Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe			
	130	135	140

Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr  
145 150 155 160

His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met  
165 170 175

Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser  
180 185 190

Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly  
195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln  
210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His  
225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met  
245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser  
260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala  
275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp  
290 295 300

<210> 77  
<211> 903  
<212> DNA  
<213> *Ostreococcus tauri*

<220>  
<221> CDS  
<222> (1)..(903)  
<223> Delta-5-Elongase

<400> 77  
atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg ttc gcc gcg tac 48  
Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr  
1 5 10 15  
gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc 96  
Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly  
20 25 30  
atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg 144  
Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg  
35 40 45  
ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga 192  
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly

124

50	55	60	
ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg			240
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met			
65	70	75	80
ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg			288
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly			
	85	90	95
atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca			336
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser			
	100	105	110
acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg			384
Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val			
	115	120	125
tgg ttg cac tac aac aac aaa tat ttg gag cta ttg gac act gtg ttc			432
Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe			
	130	135	140
atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat			480
Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr			
	145	150	155
cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg			528
His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met			
	165	170	175
gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg			576
Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser			
	180	185	190
ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc			624
Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly			
	195	200	205
att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa			672
Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln			
	210	215	220
ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac			720
Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His			
	225	230	235
tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg			768
Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met			
	245	250	255
ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg			816
Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser			
	260	265	270
cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg			864
Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala			
	275	280	285
ccc agc gtg cga cgc acg cga tct cga aaa att gac taa			903
Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp			
	290	295	300

&lt;210&gt; 78

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Ostreococcus tauri

125

&lt;400&gt; 78

Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr  
 1 5 10 15

Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly  
 20 25 30

Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg  
 35 40 45

Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly  
 50 55 60

Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met  
 65 70 75 80

Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly  
 85 90 95

Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser  
 100 105 110

Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val  
 115 120 125

Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe  
 130 135 140

Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr  
 145 150 155 160

His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met  
 165 170 175

Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser  
 180 185 190

Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly  
 195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln  
 210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His  
 225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met  
 245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser  
 260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala  
 275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp  
 290 295 300

<210> 79  
 <211> 903  
 <212> DNA  
 <213> *Ostreococcus tauri*

<220>  
 <221> CDS  
 <222> (1)..(903)  
 <223> Delta-5-Elongase

<400> 79  
 atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg tcc gcc gcg tac 48  
 Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Ser Ala Ala Tyr  
 1 5 10 15  
 gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc 96  
 Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly  
 20 25 30  
 atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg 144  
 Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg  
 35 40 45  
 ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga 192  
 Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly  
 50 55 60  
 ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg 240  
 Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met  
 65 70 75 80  
 ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg 288  
 Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly  
 85 90 95  
 atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca 336  
 Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser  
 100 105 110  
 acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg 384  
 Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val  
 115 120 125  
 tgg ttg cac tac aac aac caa tat ttg gag cta ttg gac act gtg ttc 432  
 Trp Leu His Tyr Asn Asn Gln Tyr Leu Glu Leu Leu Asp Thr Val Phe  
 130 135 140  
 atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat 480  
 Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr  
 145 150 155 160  
 cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg 528  
 His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met  
 165 170 175  
 gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg 576  
 Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser

127

180	185	190	
ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc			624
Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly			
195	200	205	
att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa			672
Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln			
210	215	220	
ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac			720
Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His			
225	230	235	240
tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg			768
Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met			
	245	250	255
ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg			816
Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser			
	260	265	270
cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg			864
Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala			
	275	280	285
ccc agc gtg cga cgc acg cga tct cga aaa att gac taa			903
Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp			
	290	295	300

<210> 80  
 <211> 300  
 <212> PRT  
 <213> Ostreococcus tauri

<400> 80

Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Ser Ala Ala Tyr			
1	5	10	15
Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly			
	20	25	30
Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg			
	35	40	45
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly			
	50	55	60
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met			
	65	70	75
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly			
	85	90	95
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser			
	100	105	110
Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val			
	115	120	125

Trp Leu His Tyr Asn Asn Gln Tyr Leu Glu Leu Leu Asp Thr Val Phe  
130 135 140

Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr  
145 150 155 160

His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met  
165 170 175

Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser  
180 185 190

Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly  
195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln  
210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His  
225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met  
245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser  
260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala  
275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp  
290 295 300

<210> 81  
<211> 879  
<212> DNA  
<213> *Ostreococcus tauri*

<220>  
<221> CDS  
<222> (1)...(879)  
<223> Delta-6-Elongase

<400> 81  
atg agt ggc tta cgt gca ccc aac ttt tta cac aga ttc tgg aca aag 48  
Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys  
1 5 10 15

tgg gac tac gcg att tcc aaa gtc gtc ttc acg tgt gcc gac agt ttt 96  
Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe  
20 25 30

cag tgg gac atc ggg cca gtg agt tcg agt acg gcg cat tta ccc gcc 144  
Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala



129

35	40	45	
att gaa tcc cct acc cca ctg gtg act agc ctc ttg ttc tac tta gtc			192
Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val			
50	55	60	
aca gtt ttc ttg tgg tat ggt cgt tta acc agg agt tca gac aag aaa			240
Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys			
65	70	75	80
att aga gag cct acg tgg tta aga aga ttc ata ata tgt cat aat gcg			288
Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala			
	85	90	95
ttc ttg ata gtc ctc agt ctt tac atg tgc ctt ggt tgt gtg gcc caa			336
Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln			
	100	105	110
gcg tat cag aat gga tat act tta tgg ggt aat gaa ttc aag gcc acg			384
Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr			
	115	120	125
gaa act cag ctt gct ctc tac att tac att ttt tac gta agt aaa ata			432
Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile			
	130	135	140
tac gag ttt gta gat act tac att atg ctt ctc aag aat aac ttg cgg			480
Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg			
	145	150	155
caa gta aga ttc cta cac act tat cac cac agc acg att tcc ttt att			528
Gln Val Arg Phe Leu His Thr Tyr His His Ser Thr Ile Ser Phe Ile			
	165	170	175
tgg tgg atc att gct cgg agg gct ccg ggt ggt gat gct tac ttc agc			576
Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser			
	180	185	190
gcg gcc ttg aac tca tgg gta cac gtg tgc atg tac acc tat tat cta			624
Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu			
	195	200	205
tta tca acc ctt att gga aaa gaa gat cct aag cgt tcc aac tac ctt			672
Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu			
	210	215	220
tgg tgg ggt cgc cac cta acg caa atg cag atg ctt cag ttt ttc ttc			720
Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe			
	225	230	235
aac gta ctt caa gcg ttg tac tgc gct tcg ttc tct acg tat ccc aag			768
Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys			
	245	250	255
ttt ttg tcc aaa att ctg ctc gtc tat atg atg agc ctt ctc ggc ttg			816
Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu			
	260	265	270
ttt ggg cat ttc tac tat tcc aag cac ata gca gca gct aag ctc cag			864
Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln			
	275	280	285
aaa aaa cag cag tga			879
Lys Lys Gln Gln			
290			

&lt;210&gt; 82

130

<211> 292  
 <212> PRT  
 <213> *Ostreococcus tauri*

<400> 82

Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys  
 1 5 10 15

Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe  
 20 25 30

Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala  
 35 40 45

Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val  
 50 55 60

Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys  
 65 70 75 80

Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala  
 85 90 95

Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln  
 100 105 110

Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr  
 115 120 125

Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile  
 130 135 140

Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg  
 145 150 155 160

Gln Val Arg Phe Leu His Thr Tyr His His Ser Thr Ile Ser Phe Ile  
 165 170 175

Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser  
 180 185 190

Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu  
 195 200 205

Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu  
 210 215 220

Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe  
 225 230 235 240

Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys  
 245 250 255

Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu  
 260 265 270

Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln  
 275 280 285

Lys Lys Gln Gln  
 290

<210> 83  
 <211> 831  
 <212> DNA  
 <213> *Thraustochytrium* sp.

<220>  
 <221> CDS  
 <222> (1)..(831)  
 <223> Delta-5-Elongase

<400> 83  
 atg gac gtc gtc gag cag caa tgg cgc cgc ttc gtg gac gcc gtg gac 48  
 Met Asp Val Val Glu Gln Gln Trp Arg Arg Phe Val Asp Ala Val Asp  
 1 5 10 15  
 aac gga atc gtg gag ttc atg gag cat gag aag ccc aac aag ctg aac 96  
 Asn Gly Ile Val Glu Phe Met Glu His Glu Lys Pro Asn Lys Leu Asn  
 20 25 30  
 gag ggc aag ctc ttc acc tcg acc gag gag atg atg gcg ctt atc gtc 144  
 Glu Gly Lys Leu Phe Thr Ser Thr Glu Glu Met Met Ala Leu Ile Val  
 35 40 45  
 ggc tac ctg gcg ttc gtg gtc ctc ggg tcc gcc ttc atg aag gcc ttt 192  
 Gly Tyr Leu Ala Phe Val Val Leu Gly Ser Ala Phe Met Lys Ala Phe  
 50 55 60  
 gtc gat aag cct ttc gag ctc aag ttc ctc aag ctc gtg cac aac atc 240  
 Val Asp Lys Pro Phe Glu Leu Lys Phe Leu Lys Leu Val His Asn Ile  
 65 70 75 80  
 ttc ctc acc ggt ctg tcc atg tac atg gcc acc gag tgc gcg cgc cag 288  
 Phe Leu Thr Gly Leu Ser Met Tyr Met Ala Thr Glu Cys Ala Arg Gln  
 85 90 95  
 gca tac ctc ggc ggc tac aag ctc ttt ggc aac ccg atg gag aag ggc 336  
 Ala Tyr Leu Gly Gly Tyr Lys Leu Phe Gly Asn Pro Met Glu Lys Gly  
 100 105 110  
 acc gag tcg cac gcc ccg ggc atg gcc aac atc atc tac atc ttc tac 384  
 Thr Glu Ser His Ala Pro Gly Met Ala Asn Ile Ile Tyr Ile Phe Tyr  
 115 120 125  
 gtg agc aag ttc ctc gaa ttc ctc gac acc gtc ttc atg atc ctc ggc 432  
 Val Ser Lys Phe Leu Glu Phe Leu Asp Thr Val Phe Met Ile Leu Gly  
 130 135 140  
 aag aag tgg aag cag ctc agc ttt ctc cac gtc tac cac cac gcg agc 480  
 Lys Lys Trp Lys Gln Leu Ser Phe Leu His Val Tyr His His Ala Ser  
 145 150 155 160  
 atc agc ttc atc tgg ggc atc atc gcc cgc ttc gcg ccc ggt ggc gac 528  
 Ile Ser Phe Ile Trp Gly Ile Ile Ala Arg Phe Ala Pro Gly Gly Asp

132

165	170	175	
gcc tac ttc tct acc atc ctc aac agc agc gtg cat gtc gtg ctc tac			576
Ala Tyr Phe Ser Thr Ile Leu Asn Ser Ser Val His Val Val Leu Tyr			
180	185	190	
ggc tac tac gcc tgc acc acc ctc ggc tac acc ttc atg cgc ccg ctg			624
Gly Tyr Tyr Ala Ser Thr Thr Leu Gly Tyr Thr Phe Met Arg Pro Leu			
195	200	205	
cgc ccg tac att acc acc att cag ctc acg cag ttc atg gcc atg gtc			672
Arg Pro Tyr Ile Thr Thr Ile Gln Leu Thr Gln Phe Met Ala Met Val			
210	215	220	
gtc cag tcc gtc tat gac tac tac aac ccc tgc gac tac ccg cag ccc			720
Val Gln Ser Val Tyr Asp Tyr Tyr Asn Pro Cys Asp Tyr Pro Gln Pro			
225	230	235	240
ctc gtc aag ctg ctc ttc tgg tac atg ctc acc atg ctc ggc ctc ttc			768
Leu Val Lys Leu Leu Phe Trp Tyr Met Leu Thr Met Leu Gly Leu Phe			
245	250	255	
ggc aac ttc ttc gtg cag cag tac ctc aag ccc aag gcg ccc aag aag			816
Gly Asn Phe Phe Val Gln Gln Tyr Leu Lys Pro Lys Ala Pro Lys Lys			
260	265	270	
cag aag acc atc taa			831
Gln Lys Thr Ile			
275			
<210>	84		
<211>	276		
<212>	PRT		
<213>	Thraustochytrium sp.		
<400>	84		
Met Asp Val Val Glu Gln Gln Trp Arg Arg Phe Val Asp Ala Val Asp			
1	5	10	15
Asn Gly Ile Val Glu Phe Met Glu His Glu Lys Pro Asn Lys Leu Asn			
20	25	30	
Glu Gly Lys Leu Phe Thr Ser Thr Glu Glu Met Met Ala Leu Ile Val			
35	40	45	
Gly Tyr Leu Ala Phe Val Val Leu Gly Ser Ala Phe Met Lys Ala Phe			
50	55	60	
Val Asp Lys Pro Phe Glu Leu Lys Phe Leu Lys Leu Val His Asn Ile			
65	70	75	80
Phe Leu Thr Gly Leu Ser Met Tyr Met Ala Thr Glu Cys Ala Arg Gln			
85	90	95	
Ala Tyr Leu Gly Gly Tyr Lys Leu Phe Gly Asn Pro Met Glu Lys Gly			
100	105	110	
Thr Glu Ser His Ala Pro Gly Met Ala Asn Ile Ile Tyr Ile Phe Tyr			
115	120	125	

Val Ser Lys Phe Leu Glu Phe Leu Asp Thr Val Phe Met Ile Leu Gly  
130 135 140

Lys Lys Trp Lys Gln Leu Ser Phe Leu His Val Tyr His His Ala Ser  
145 150 155 160

Ile Ser Phe Ile Trp Gly Ile Ile Ala Arg Phe Ala Pro Gly Gly Asp  
165 170 175

Ala Tyr Phe Ser Thr Ile Leu Asn Ser Ser Val His Val Val Leu Tyr  
180 185 190

Gly Tyr Tyr Ala Ser Thr Thr Leu Gly Tyr Thr Phe Met Arg Pro Leu  
195 200 205

Arg Pro Tyr Ile Thr Thr Ile Gln Leu Thr Gln Phe Met Ala Met Val  
210 215 220

Val Gln Ser Val Tyr Asp Tyr Tyr Asn Pro Cys Asp Tyr Pro Gln Pro  
225 230 235 240

Leu Val Lys Leu Leu Phe Trp Tyr Met Leu Thr Met Leu Gly Leu Phe  
245 250 255

Gly Asn Phe Phe Val Gln Gln Tyr Leu Lys Pro Lys Ala Pro Lys Lys  
260 265 270

Gln Lys Thr Ile  
275

<210> 85  
<211> 1077  
<212> DNA  
<213> *Thalassiosira pseudonana*

<220>  
<221> CDS  
<222> (1)..(1077)  
<223> Delta-5-Elongase

<400> 85  
atg tgc tca cca ccg ccg tca caa tcc aaa aca aca tcc ctc cta gca 48  
Met Cys Ser Pro Pro Pro Ser Gln Ser Lys Thr Thr Ser Leu Leu Ala  
1 5 10 15

cgg tac acc acc gcc gcc ctc ctc ctc ctc acc ctc aca acg tgg tgc 96  
Arg Tyr Thr Thr Ala Ala Leu Leu Leu Leu Thr Leu Thr Thr Trp Cys  
20 25 30

cac ttc gcc ttc cca gcc gcc acc gcc aca ccc ggc ctc acc gcc gaa 144  
His Phe Ala Phe Pro Ala Ala Thr Ala Thr Pro Gly Leu Thr Ala Glu  
35 40 45

atg cac tcc tac aaa gtc cca ctc ggt ctc acc gta ttc tac ctg ctg 192  
Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu

50	55	60	
agt cta ccg tca cta aag tac gtt acg gac aac tac ctt gcc aaa aag Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys 65 70 75 80			240
tat gat atg aag tca ctc ctg acg gaa tca atg gtg ttg tac aat gtg Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val 85 90 95			288
gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala 100 105 110			336
gtg atg aat aga gac cat cct ttt att gga agt aga agt ttg gtt ggg Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly 115 120 125			384
gcg gcg ttg cat agt ggg agc tcg tat gcg gtg tgg gtt cat tat tgt Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys 130 135 140			432
gat aag tat ttg gag ttc ttt gat acg tat ttt atg gtg ttg agg ggg Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly 145 150 155 160			480
aaa atg gac cag gtc tcc ttc ctc cac atc tac cac cac acg acc ata Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile 165 170 175			528
gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggc gga gac att Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile 180 185 190			576
tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc atg tat tcc Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser 195 200 205			624
tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg aaa cga tac Tyr Tyr Ala Leu Ala Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr 210 215 220			672
ttg act caa gct caa tta ttg caa ttc aca agt gtg gtg gtt tat acg Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr 225 230 235 240			720
ggg tgt acg ggt tat act cat tac tat cat acg aag cat gga gcg gat Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp 245 250 255			768
gag aca cag cct agt tta gga acg tat tat ttc tgt tgt gga gtg cag Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln 260 265 270			816
gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc ttt tat aaa Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys 275 280 285			864
cga tcc tat tcg aag aag aac aag tca gga gga aag gat agc aag aag Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys 290 295 300			912
aat gat gat ggg aat aat gag gat caa tgt cac aag gct atg aag gat Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp 305 310 315 320			960
ata tcg gag ggt gcg aag gag gtt gtg ggg cat gca gcg aag gat gct Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala			1008

## 135

325 330 335  
 gga aag ttg gtg gct acg gcg agt aag gct gta aag agg aag gga act 1056  
 Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr  
 340 345 350  
 cgt gtt act ggt gcc atg tag 1077  
 Arg Val Thr Gly Ala Met  
 355  
  
 <210> 86  
 <211> 358  
 <212> PRT  
 <213> *Thalassiosira pseudonana*  
  
 <400> 86  
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 1 5 10 15  
 Arg Tyr Thr Thr Ala Ala Leu Leu Leu Leu Thr Leu Thr Thr Trp Cys  
 20 25 30  
 His Phe Ala Phe Pro Ala Ala Thr Ala Thr Pro Gly Leu Thr Ala Glu  
 35 40 45  
 Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu  
 50 55 60  
 Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys  
 65 70 75 80  
 Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val  
 85 90 95  
 Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala  
 100 105 110  
 Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly  
 115 120 125  
 Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys  
 130 135 140  
 Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly  
 145 150 155 160  
 Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile  
 165 170 175  
 Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile  
 180 185 190  
 Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser  
 195 200 205

Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr  
 210 215 220

Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr  
 225 230 235 240

Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp  
 245 250 255

Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln  
 260 265 270

Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys  
 275 280 285

Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys  
 290 295 300

Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp  
 305 310 315 320

Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala  
 325 330 335

Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr  
 340 345 350

Arg Val Thr Gly Ala Met  
 355

<210> 87  
 <211> 1086  
 <212> DNA  
 <213> *Phytophthora infestans*

<220>  
 <221> CDS  
 <222> (1)..(1086)  
 <223> Omega-3-Desaturase

<400> 87  
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 Met Ala Thr Lys Glu Ala Tyr Val Phe Pro Thr Leu Thr Glu Ile Lys  
 1 5 10 15

cgg tcg cta cct aaa gac tgt ttc gag gct tcg gtg cct ctg tcg ctc 96  
 Arg Ser Leu Pro Lys Asp Cys Phe Glu Ala Ser Val Pro Leu Ser Leu  
 20 25 30

tac tac acc gtg cgt tgt ctg gtg atc gcg gtg gct cta acc ttc ggt 144  
 Tyr Tyr Thr Val Arg Cys Leu Val Ile Ala Val Ala Leu Thr Phe Gly  
 35 40 45

ctc aac tac gct cgc gct ctg ccc gag gtc gag agc ttc tgg gct ctg 192  
 Leu Asn Tyr Ala Arg Ala Leu Pro Glu Val Glu Ser Phe Trp Ala Leu



50	55	60	
gac gcc gca ctc tgc acg ggc tac atc ttg ctg cag ggc atc gtg ttc Asp Ala Ala Leu Cys Thr Gly Tyr Ile Leu Leu Gln Gly Ile Val Phe 65 70 75 80			240
tgg ggc ttc ttc acg gtg ggc cac gat gcc ggc cac ggc gcc ttc tcg Trp Gly Phe Phe Thr Val Gly His Asp Ala Gly His Gly Ala Phe Ser 85 90 95			288
cgc tac cac ctg ctt aac ttc gtg gtg ggc act ttc atg cac tcg ctc Arg Tyr His Leu Leu Asn Phe Val Val Gly Thr Phe Met His Ser Leu 100 105 110			336
atc ctc acg ccc ttc gag tcg tgg aag ctc acg cac cgt cac cac cac Ile Leu Thr Pro Phe Glu Ser Trp Lys Leu Thr His Arg His His His 115 120 125			384
aag aac acg ggc aac att gac cgt gac gag gtc ttc tac ccg caa cgc Lys Asn Thr Gly Asn Ile Asp Arg Asp Glu Val Phe Tyr Pro Gln Arg 130 135 140			432
aag gcc gac gac cac ccg ctg tct cgc aac ctg att ctg gcg ctc ggg Lys Ala Asp Asp His Pro Leu Ser Arg Asn Leu Ile Leu Ala Leu Gly 145 150 155 160			480
gca gcg tgg ctc gcc tat ttg gtc gag ggc ttc cct cct cgt aag gtc Ala Ala Trp Leu Ala Tyr Leu Val Glu Gly Phe Pro Pro Arg Lys Val 165 170 175			528
aac cac ttc aac ccg ttc gag cct ctg ttc gtg cgt cag gtg tca gct Asn His Phe Asn Pro Phe Glu Pro Leu Phe Val Arg Gln Val Ser Ala 180 185 190			576
gtg gta atc tct ctt ctc gcc cac ttc ttc gtg gcc gga ctc tcc atc Val Val Ile Ser Leu Leu Ala His Phe Phe Val Ala Gly Leu Ser Ile 195 200 205			624
tat ctg agc ctc cag ctg ggc ctt aag acg atg gca atc tac tac tat Tyr Leu Ser Leu Gln Leu Gly Leu Lys Thr Met Ala Ile Tyr Tyr Tyr 210 215 220			672
gga cct gtt ttt gtg ttc ggc agc atg ctg gtc att acc acc ttc cta Gly Pro Val Phe Val Phe Gly Ser Met Leu Val Ile Thr Thr Phe Leu 225 230 235 240			720
cac cac aat gat gag gag acc cca tgg tac gcc gac tcg gag tgg acg His His Asn Asp Glu Glu Thr Pro Trp Tyr Ala Asp Ser Glu Trp Thr 245 250 255			768
tac gtc aag ggc aac ctc tcg tcc gtg gac cga tcg tac ggc gcg ctc Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala Leu 260 265 270			816
att gac aac ctg agc cac aac atc ggc acg cac cag atc cac cac ctt Ile Asp Asn Leu Ser His Asn Ile Gly Thr His Gln Ile His His Leu 275 280 285			864
ttc cct atc att ccg cac tac aaa ctc aag aaa gcc act gcg gcc ttc Phe Pro Ile Ile Pro His Tyr Lys Leu Lys Lys Ala Thr Ala Ala Phe 290 295 300			912
cac cag gct ttc cct gag ctc gtg cgc aag agc gac gag cca att atc His Gln Ala Phe Pro Glu Leu Val Arg Lys Ser Asp Glu Pro Ile Ile 305 310 315 320			960
aag gct ttc ttc cgg gtt gga cgt ctc tac gca aac tac ggc gtt gtg Lys Ala Phe Phe Arg Val Gly Arg Leu Tyr Ala Asn Tyr Gly Val Val			1008

325 330 335  
 gac cag gag gcg aag ctc ttc acg cta aag gaa gcc aag gcg gcg acc 1056  
 Asp Gln Glu Ala Lys Leu Phe Thr Leu Lys Glu Ala Lys Ala Ala Thr  
 340 345 350  
 gag gcg gcg gcc aag acc aag tcc acg taa 1086  
 Glu Ala Ala Ala Lys Thr Lys Ser Thr  
 355 360  
 <210> 88  
 <211> 361  
 <212> PRT  
 <213> *Phytophthora infestans*  
 <400> 88  
 Met Ala Thr Lys Glu Ala Tyr Val Phe Pro Thr Leu Thr Glu Ile Lys  
 1 5 10 15  
 Arg Ser Leu Pro Lys Asp Cys Phe Glu Ala Ser Val Pro Leu Ser Leu  
 20 25 30  
 Tyr Tyr Thr Val Arg Cys Leu Val Ile Ala Val Ala Leu Thr Phe Gly  
 35 40 45  
 Leu Asn Tyr Ala Arg Ala Leu Pro Glu Val Glu Ser Phe Trp Ala Leu  
 50 55 60  
 Asp Ala Ala Leu Cys Thr Gly Tyr Ile Leu Leu Gln Gly Ile Val Phe  
 65 70 75 80  
 Trp Gly Phe Phe Thr Val Gly His Asp Ala Gly His Gly Ala Phe Ser  
 85 90 95  
 Arg Tyr His Leu Leu Asn Phe Val Val Gly Thr Phe Met His Ser Leu  
 100 105 110  
 Ile Leu Thr Pro Phe Glu Ser Trp Lys Leu Thr His Arg His His His  
 115 120 125  
 Lys Asn Thr Gly Asn Ile Asp Arg Asp Glu Val Phe Tyr Pro Gln Arg  
 130 135 140  
 Lys Ala Asp Asp His Pro Leu Ser Arg Asn Leu Ile Leu Ala Leu Gly  
 145 150 155 160  
 Ala Ala Trp Leu Ala Tyr Leu Val Glu Gly Phe Pro Pro Arg Lys Val  
 165 170 175  
 Asn His Phe Asn Pro Phe Glu Pro Leu Phe Val Arg Gln Val Ser Ala  
 180 185 190  
 Val Val Ile Ser Leu Leu Ala His Phe Phe Val Ala Gly Leu Ser Ile  
 195 200 205

Tyr Leu Ser Leu Gln Leu Gly Leu Lys Thr Met Ala Ile Tyr Tyr Tyr  
 210 215 220

Gly Pro Val Phe Val Phe Gly Ser Met Leu Val Ile Thr Thr Phe Leu  
 225 230 235 240

His His Asn Asp Glu Glu Thr Pro Trp Tyr Ala Asp Ser Glu Trp Thr  
 245 250 255

Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala Leu  
 260 265 270

Ile Asp Asn Leu Ser His Asn Ile Gly Thr His Gln Ile His His Leu  
 275 280 285

Phe Pro Ile Ile Pro His Tyr Lys Leu Lys Lys Ala Thr Ala Ala Phe  
 290 295 300

His Gln Ala Phe Pro Glu Leu Val Arg Lys Ser Asp Glu Pro Ile Ile  
 305 310 315 320

Lys Ala Phe Phe Arg Val Gly Arg Leu Tyr Ala Asn Tyr Gly Val Val  
 325 330 335

Asp Gln Glu Ala Lys Leu Phe Thr Leu Lys Glu Ala Lys Ala Ala Thr  
 340 345 350

Glu Ala Ala Ala Lys Thr Lys Ser Thr  
 355 360

<210> 89  
 <211> 1371  
 <212> DNA  
 <213> *Ostreococcus tauri*

<220>  
 <221> CDS  
 <222> (1)..(1371)  
 <223> Delta-6-Desaturase

<400> 89  
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gcg ttc gac ggt gag cgc gag cgg gcg gag gca aac gtg aag ctg tcc 96  
 Ala Phe Asp Gly Glu Arg Glu Arg Ala Glu Ala Asn Val Lys Leu Ser  
 20 25 30

gcg gag aag atg gag ccg gcg gcg ctg gcg aag acg ttc gcg agg cgg 144  
 Ala Glu Lys Met Glu Pro Ala Ala Leu Ala Lys Thr Phe Ala Arg Arg  
 35 40 45

tac gtc gtg atc gag ggg gtg gag tac gat gtg acg gat ttt aag cac 192  
 Tyr Val Val Ile Glu Gly Val Glu Tyr Asp Val Thr Asp Phe Lys His

50	55	60	
ccg gga gga acg gtt att ttc tat gcg ttg tca aac acc ggg gcg gac Pro Gly Gly Thr Val Ile Phe Tyr Ala Leu Ser Asn Thr Gly Ala Asp 65 70 75 80			240
gcg acg gaa gcg ttc aag gag ttt cat cat cgg tcg aga aag gcg agg Ala Thr Glu Ala Phe Lys Glu Phe His His Arg Ser Arg Lys Ala Arg 85 90 95			288
aaa gcc ttg gcg gcg ctc ccg tct cga ccg gcc aag acg gcc aag gtg Lys Ala Leu Ala Ala Leu Pro Ser Arg Pro Ala Lys Thr Ala Lys Val 100 105 110			336
gac gac gcg gag atg ctc caa gat ttc gcc aag tgg cgg aaa gaa ttg Asp Asp Ala Glu Met Leu Gln Asp Phe Ala Lys Trp Arg Lys Glu Leu 115 120 125			384
gag aga gat gga ttc ttc aag ccc tct ccg gcg cac gtg gcg tat cgc Glu Arg Asp Gly Phe Phe Lys Pro Ser Pro Ala His Val Ala Tyr Arg 130 135 140			432
ttc gcc gag ctc gcg gcg atg tac gct ctc ggg acg tac ctg atg tac Phe Ala Glu Leu Ala Ala Met Tyr Ala Leu Gly Thr Tyr Leu Met Tyr 145 150 155 160			480
gct cga tac gtc gtc tcc tcg gtg ctc gtg tac gct tgc ttt ttc ggc Ala Arg Tyr Val Val Ser Ser Val Leu Val Tyr Ala Cys Phe Phe Gly 165 170 175			528
gcc cga tgc ggt tgg gtg cag cac gag ggc gga cac agc tcg ctg acg Ala Arg Cys Gly Trp Val Gln His Glu Gly Gly His Ser Ser Leu Thr 180 185 190			576
ggc aac att tgg tgg gac aag cgc atc cag gcc ttc aca gcc ggg ttc Gly Asn Ile Trp Trp Asp Lys Arg Ile Gln Ala Phe Thr Ala Gly Phe 195 200 205			624
ggt ctc gcc ggt agc ggc gac atg tgg aac tcg atg cac aac aag cat Gly Leu Ala Gly Ser Gly Asp Met Trp Asn Ser Met His Asn Lys His 210 215 220			672
cac gcg acg cct caa aag gtt cgt cac gac atg gat ctg gac acc acc His Ala Thr Pro Gln Lys Val Arg His Asp Met Asp Leu Asp Thr Thr 225 230 235 240			720
ccc gcg gtg gcg ttc ttc aac acc gcg gtg gaa gac aat cgt ccc cgt Pro Ala Val Ala Phe Phe Asn Thr Ala Val Glu Asp Asn Arg Pro Arg 245 250 255			768
ggc ttt agc aag tac tgg ttg cgc ctt cag gcg tgg acc ttc atc ccc Gly Phe Ser Lys Tyr Trp Leu Arg Leu Gln Ala Trp Thr Phe Ile Pro 260 265 270			816
gtg acg tcc ggc ttg gtg ctc ctt ttc tgg atg ttt ttc ctc cac ccc Val Thr Ser Gly Leu Val Leu Leu Phe Trp Met Phe Phe Leu His Pro 275 280 285			864
tcc aag gct ttg aag ggt ggc aag tac gaa gag ttg gtg tgg atg ctc Ser Lys Ala Leu Lys Gly Gly Lys Tyr Glu Glu Leu Val Trp Met Leu 290 295 300			912
gcc gcg cac gtc atc cgc acg tgg acg atc aag gcg gtg acc gga ttc Ala Ala His Val Ile Arg Thr Trp Thr Ile Lys Ala Val Thr Gly Phe 305 310 315 320			960
acc gcg atg cag tcc tac ggc tta ttt ttg gcg acg agc tgg gtg agc Thr Ala Met Gln Ser Tyr Gly Leu Phe Leu Ala Thr Ser Trp Val Ser 1008			

141

325	330	335	
ggc tgc tat ctg ttt gca cac ttc tcc acg tcg cac acg cac ctg gat			1056
Gly Cys Tyr Leu Phe Ala His Phe Ser Thr Ser His Thr His Leu Asp			
340	345	350	
gtg gtg ccc gcg gac gag cat ctc tcc tgg gtt cga tac gcc gtc gat			1104
Val Val Pro Ala Asp Glu His Leu Ser Trp Val Arg Tyr Ala Val Asp			
355	360	365	
cac acg atc gac atc gat ccg agt caa ggt tgg gtg aac tgg ttg atg			1152
His Thr Ile Asp Ile Asp Pro Ser Gln Gly Trp Val Asn Trp Leu Met			
370	375	380	
ggc tac ctc aac tgc caa gtc atc cac cac ctc ttt ccg agc atg ccg			1200
Gly Tyr Leu Asn Cys Gln Val Ile His His Leu Phe Pro Ser Met Pro			
385	390	400	
cag ttc cgc cag ccc gag gta tct cgc cgc ttc gtc gcc ttt gcg aaa			1248
Gln Phe Arg Gln Pro Glu Val Ser Arg Arg Phe Val Ala Phe Ala Lys			
405	410	415	
aag tgg aac ctc aac tac aag gtc atg acc tac gcc ggt gcg tgg aag			1296
Lys Trp Asn Leu Asn Tyr Lys Val Met Thr Tyr Ala Gly Ala Trp Lys			
420	425	430	
gca acg ctc gga aac ctc gac aac gtg ggt aag cac tac tac gtg cac			1344
Ala Thr Leu Gly Asn Leu Asp Asn Val Gly Lys His Tyr Tyr Val His			
435	440	445	
ggc caa cac tcc gga aag acg gcg taa			1371
Gly Gln His Ser Gly Lys Thr Ala			
450	455		

&lt;210&gt; 90

&lt;211&gt; 456

&lt;212&gt; PRT

<213> *Ostreococcus tauri*

&lt;400&gt; 90

Met Cys Val Glu Thr Glu Asn Asn Asp Gly Ile Pro Thr Val Glu Ile
1 5 10 15

Ala Phe Asp Gly Glu Arg Glu Arg Ala Glu Ala Asn Val Lys Leu Ser
20 25 30

Ala Glu Lys Met Glu Pro Ala Ala Leu Ala Lys Thr Phe Ala Arg Arg
35 40 45

Tyr Val Val Ile Glu Gly Val Glu Tyr Asp Val Thr Asp Phe Lys His
50 55 60

Pro Gly Gly Thr Val Ile Phe Tyr Ala Leu Ser Asn Thr Gly Ala Asp
65 70 75 80

Ala Thr Glu Ala Phe Lys Glu Phe His His Arg Ser Arg Lys Ala Arg
85 90 95

Lys Ala Leu Ala Ala Leu Pro Ser Arg Pro Ala Lys Thr Ala Lys Val
100 105 110

Asp Asp Ala Glu Met Leu Gln Asp Phe Ala Lys Trp Arg Lys Glu Leu  
 115 120 125

Glu Arg Asp Gly Phe Phe Lys Pro Ser Pro Ala His Val Ala Tyr Arg  
 130 135 140

Phe Ala Glu Leu Ala Ala Met Tyr Ala Leu Gly Thr Tyr Leu Met Tyr  
 145 150 155 160

Ala Arg Tyr Val Val Ser Ser Val Leu Val Tyr Ala Cys Phe Phe Gly  
 165 170 175

Ala Arg Cys Gly Trp Val Gln His Glu Gly Gly His Ser Ser Leu Thr  
 180 185 190

Gly Asn Ile Trp Trp Asp Lys Arg Ile Gln Ala Phe Thr Ala Gly Phe  
 195 200 205

Gly Leu Ala Gly Ser Gly Asp Met Trp Asn Ser Met His Asn Lys His  
 210 215 220

His Ala Thr Pro Gln Lys Val Arg His Asp Met Asp Leu Asp Thr Thr  
 225 230 235 240

Pro Ala Val Ala Phe Phe Asn Thr Ala Val Glu Asp Asn Arg Pro Arg  
 245 250 255

Gly Phe Ser Lys Tyr Trp Leu Arg Leu Gln Ala Trp Thr Phe Ile Pro  
 260 265 270

Val Thr Ser Gly Leu Val Leu Leu Phe Trp Met Phe Phe Leu His Pro  
 275 280 285

Ser Lys Ala Leu Lys Gly Gly Lys Tyr Glu Glu Leu Val Trp Met Leu  
 290 295 300

Ala Ala His Val Ile Arg Thr Trp Thr Ile Lys Ala Val Thr Gly Phe  
 305 310 315 320

Thr Ala Met Gln Ser Tyr Gly Leu Phe Leu Ala Thr Ser Trp Val Ser  
 325 330 335

Gly Cys Tyr Leu Phe Ala His Phe Ser Thr Ser His Thr His Leu Asp  
 340 345 350

Val Val Pro Ala Asp Glu His Leu Ser Trp Val Arg Tyr Ala Val Asp  
 355 360 365

His Thr Ile Asp Ile Asp Pro Ser Gln Gly Trp Val Asn Trp Leu Met  
 370 375 380

Gly Tyr Leu Asn Cys Gln Val Ile His His Leu Phe Pro Ser Met Pro  
385 390 395 400

Gln Phe Arg Gln Pro Glu Val Ser Arg Arg Phe Val Ala Phe Ala Lys  
405 410 415

Lys Trp Asn Leu Asn Tyr Lys Val Met Thr Tyr Ala Gly Ala Trp Lys  
420 425 430

Ala Thr Leu Gly Asn Leu Asp Asn Val Gly Lys His Tyr Tyr Val His  
435 440 445

Gly Gln His Ser Gly Lys Thr Ala  
450 455

<210> 91  
<211> 606  
<212> DNA  
<213> *Ostreococcus tauri*

<220>  
<221> CDS  
<222> (1)..(606).  
<223> Delta-5-Desaturase

<400> 91  
atg tac ggt ttg cta tcg ctc aag tcg tgc ttc gtc gac gat ttc aac 48  
Met Tyr Gly Leu Leu Ser Leu Lys Ser Cys Phe Val Asp Asp Phe Asn  
1 5 10 15  
gcc tac ttc tcc gga cgc atc ggc tgg gtc aag gtg atg aag ttc acc 96  
Ala Tyr Phe Ser Gly Arg Ile Gly Trp Val Lys Val Met Lys Phe Thr  
20 25 30  
cgc ggc gag gcg atc gca ttt tgg ggc acc aag ctc ttg tgg gcc gcg 144  
Arg Gly Glu Ala Ile Ala Phe Trp Gly Thr Lys Leu Leu Trp Ala Ala  
35 40 45  
tat tac ctc gcg ttg ccg cta aag atg tcg cat cgg ccg ctc gga gaa 192  
Tyr Tyr Leu Ala Leu Pro Leu Lys Met Ser His Arg Pro Leu Gly Glu  
50 55 60  
ctc ctc gca ctc tgg gcc gtc acc gag ttc gtc acc gga tgg ctg ttg 240  
Leu Leu Ala Leu Trp Ala Val Thr Glu Phe Val Thr Gly Trp Leu Leu  
65 70 75 80  
gcg ttc atg ttc caa gtc gcc cac gtc gtc ggc gag gtt cac ttc ttc 288  
Ala Phe Met Phe Gln Val Ala His Val Val Gly Glu Val His Phe Phe  
85 90 95  
acc ctc gac gcg aag aac cgc gtg aac ttg gga tgg gga gag gca cag 336  
Thr Leu Asp Ala Lys Asn Arg Val Asn Leu Gly Trp Gly Glu Ala Gln  
100 105 110  
ctc atg tcg agc gcg gat ttc gcc cac gga tcc aag ttt tgg acg cac 384  
Leu Met Ser Ser Ala Asp Phe Ala His Gly Ser Lys Phe Trp Thr His  
115 120 125  
ttc tcc gga ggc tta aac tac caa gtc gtc cac cat ctc ttc ccg gcc 432  
Phe Ser Gly Gly Leu Asn Tyr Gln Val Val His His Leu Phe Pro Gly

144

130                      135                      140  
 gtc tgc cac gtg cac tat ccc gcg ctc gcg cca att att aag gcg gca      480  
 Val Cys His Val His Tyr Pro Ala Leu Ala Pro Ile Ile Lys Ala Ala  
 145                      150                      155                      160  
 gct gag aag cac ggc ctc cac tac cag att tac ccc acg ttt tgg tcc      528  
 Ala Glu Lys His Gly Leu His Tyr Gln Ile Tyr Pro Thr Phe Trp Ser  
                     165                      170                      175  
 gcc ctg cgc gcg cac ttc cgg cac ctc gcc aac gtc ggc cgc gcc gcg      576  
 Ala Leu Arg Ala His Phe Arg His Leu Ala Asn Val Gly Arg Ala Ala  
                     180                      185                      190  
 tac gta ccg tcc ctc caa acc gtc gga tga      606  
 Tyr Val Pro Ser Leu Gln Thr Val Gly  
                     195                      200  
  
 <210> 92  
 <211> 201  
 <212> PRT  
 <213> *Ostreococcus tauri*  
  
 <400> 92  
 Met Tyr Gly Leu Leu Ser Leu Lys Ser Cys Phe Val Asp Asp Phe Asn  
 1                      5                      10                      15  
 Ala Tyr Phe Ser Gly Arg Ile Gly Trp Val Lys Val Met Lys Phe Thr  
                     20                      25                      30  
 Arg Gly Glu Ala Ile Ala Phe Trp Gly Thr Lys Leu Leu Trp Ala Ala  
                     35                      40                      45  
 Tyr Tyr Leu Ala Leu Pro Leu Lys Met Ser His Arg Pro Leu Gly Glu  
                     50                      55                      60  
 Leu Leu Ala Leu Trp Ala Val Thr Glu Phe Val Thr Gly Trp Leu Leu  
 65                      70                      75                      80  
 Ala Phe Met Phe Gln Val Ala His Val Val Gly Glu Val His Phe Phe  
                     85                      90                      95  
 Thr Leu Asp Ala Lys Asn Arg Val Asn Leu Gly Trp Gly Glu Ala Gln  
                     100                      105                      110  
 Leu Met Ser Ser Ala Asp Phe Ala His Gly Ser Lys Phe Trp Thr His  
                     115                      120                      125  
 Phe Ser Gly Gly Leu Asn Tyr Gln Val Val His His Leu Phe Pro Gly  
                     130                      135                      140  
 Val Cys His Val His Tyr Pro Ala Leu Ala Pro Ile Ile Lys Ala Ala  
 145                      150                      155                      160  
 Ala Glu Lys His Gly Leu His Tyr Gln Ile Tyr Pro Thr Phe Trp Ser  
                     165                      170                      175



Ala Leu Arg Ala His Phe Arg His Leu Ala Asn Val Gly Arg Ala Ala  
 180 185 190

Tyr Val Pro Ser Leu Gln Thr Val Gly  
 195 200

<210> 93

<211> 714

<212> DNA

<213> *Ostreococcus tauri*

<220>

<221> CDS

<222> (1)..(714)

<223> Delta-5-Desaturase

<400> 93

atg gtg agc cat cac tcg tac tgt aac gac gcg gat ttg gat cag gat 48  
 Met Val Ser His His Ser Tyr Cys Asn Asp Ala Asp Leu Asp Gln Asp  
 1 5 10 15

gtg tac acc gca ctg ccg ctc ctg cgc ctg gac ccg tct cag gag ttg 96  
 Val Tyr Thr Ala Leu Pro Leu Leu Arg Leu Asp Pro Ser Gln Glu Leu  
 20 25 30

aag tgg ttt cat cga tac cag gcg ttt tac gcc ccg ctc atg tgg ccg 144  
 Lys Trp Phe His Arg Tyr Gln Ala Phe Tyr Ala Pro Leu Met Trp Pro  
 35 40 45

ttt ttg tgg ctc gcg gcg cag ttt ggc gac gcg cag aac atc ctg atc 192  
 Phe Leu Trp Leu Ala Ala Gln Phe Gly Asp Ala Gln Asn Ile Leu Ile  
 50 55 60

gac cga gcg tcg ccg ggc gtc gcg tac aag gga ttg atg gcg aac gag 240  
 Asp Arg Ala Ser Pro Gly Val Ala Tyr Lys Gly Leu Met Ala Asn Glu  
 65 70 75 80

gtc gcg ctg tac gtt ctc ggt aag gtt tta cac ttt ggt ctt ctc ctc 288  
 Val Ala Leu Tyr Val Leu Gly Lys Val Leu His Phe Gly Leu Leu Leu  
 85 90 95

ggc gtt cct gcg tac ttg cac gga ttg tcc aac gcg atc gtt cca ttc 336  
 Gly Val Pro Ala Tyr Leu His Gly Leu Ser Asn Ala Ile Val Pro Phe  
 100 105 110

ttg gcg tac ggc gca ttc ggc tcc ttc gtc ctg tgc tgg ttc ttc atc 384  
 Leu Ala Tyr Gly Ala Phe Gly Ser Phe Val Leu Cys Trp Phe Phe Ile  
 115 120 125

gtc agc cat aac ctc gaa gcg ctg aca ccc gtt aac ctt aac aag tcc 432  
 Val Ser His Asn Leu Glu Ala Leu Thr Pro Val Asn Leu Asn Lys Ser  
 130 135 140

acg aag aac gac tgg ggg gcg tgg cag atc gag aca tcg gcg tct tgg 480  
 Thr Lys Asn Asp Trp Gly Ala Trp Gln Ile Glu Thr Ser Ala Ser Trp  
 145 150 155 160

ggc aac gcg ttc tgg agc ttc ttc tct gga ggt ctg aac ctg caa atc 528  
 Gly Asn Ala Phe Trp Ser Phe Phe Ser Gly Gly Leu Asn Leu Gln Ile  
 165 170 175

gag cac cac ctc ttc ccg ggc atg gcg cac aac ctg tac ccg aag atg 576  
 Glu His His Leu Phe Pro Gly Met Ala His Asn Leu Tyr Pro Lys Met

146

180	185	190	
gtg ccg atc atc aag gac gag tgt gcg aaa gcg ggc gtt cgc tac acc			624
Val Pro Ile Ile Lys Asp Glu Cys Ala Lys Ala Gly Val Arg Tyr Thr			
195	200	205	
ggt tac ggt ggc tac acc ggc ctg ctc ccg atc acc cgc gac atg ttc			672
Gly Tyr Gly Gly Tyr Thr Gly Leu Leu Pro Ile Thr Arg Asp Met Phe			
210	215	220	
tcc tac ctc cat aag tgt ggc cga acg gcg aaa cta gcc taa			714
Ser Tyr Leu His Lys Cys Gly Arg Thr Ala Lys Leu Ala			
225	230	235	
<210> 94			
<211> 237			
<212> PRT			
<213> Ostreococcus tauri			
<400> 94			
Met Val Ser His His Ser Tyr Cys Asn Asp Ala Asp Leu Asp Gln Asp			
1	5	10	15
Val Tyr Thr Ala Leu Pro Leu Leu Arg Leu Asp Pro Ser Gln Glu Leu			
20	25	30	
Lys Trp Phe His Arg Tyr Gln Ala Phe Tyr Ala Pro Leu Met Trp Pro			
35	40	45	
Phe Leu Trp Leu Ala Ala Gln Phe Gly Asp Ala Gln Asn Ile Leu Ile			
50	55	60	
Asp Arg Ala Ser Pro Gly Val Ala Tyr Lys Gly Leu Met Ala Asn Glu			
65	70	75	80
Val Ala Leu Tyr Val Leu Gly Lys Val Leu His Phe Gly Leu Leu Leu			
85	90	95	
Gly Val Pro Ala Tyr Leu His Gly Leu Ser Asn Ala Ile Val Pro Phe			
100	105	110	
Leu Ala Tyr Gly Ala Phe Gly Ser Phe Val Leu Cys Trp Phe Phe Ile			
115	120	125	
Val Ser His Asn Leu Glu Ala Leu Thr Pro Val Asn Leu Asn Lys Ser			
130	135	140	
Thr Lys Asn Asp Trp Gly Ala Trp Gln Ile Glu Thr Ser Ala Ser Trp			
145	150	155	160
Gly Asn Ala Phe Trp Ser Phe Phe Ser Gly Gly Leu Asn Leu Gln Ile			
165	170	175	
Glu His His Leu Phe Pro Gly Met Ala His Asn Leu Tyr Pro Lys Met			
180	185	190	

Val Pro Ile Ile Lys Asp Glu Cys Ala Lys Ala Gly Val Arg Tyr Thr  
 195 200 205

Gly Tyr Gly Gly Tyr Thr Gly Leu Leu Pro Ile Thr Arg Asp Met Phe  
 210 215 220

Ser Tyr Leu His Lys Cys Gly Arg Thr Ala Lys Leu Ala  
 225 230 235

<210> 95  
 <211> 1611  
 <212> DNA  
 <213> *Ostreococcus tauri*

<220>  
 <221> CDS  
 <222> (1)..(1611)  
 <223> Delta-4-Desaturase

<400> 95  
 atg tac ctc gga cgc ggc cgt ctc gag agc ggg acg acg cga ggg atg 48  
 Met Tyr Leu Gly Arg Gly Arg Leu Glu Ser Gly Thr Thr Arg Gly Met  
 1 5 10 15  
 atg cgg acg cac gcg cgg cga ccg tcg acg acg tcg aat ccg tgc gcg 96  
 Met Arg Thr His Ala Arg Arg Pro Ser Thr Thr Ser Asn Pro Cys Ala  
 20 25 30  
 cgg tca cgc gtg cgt aag acg acg gag cga tcg ctc gcg cga gtg cga 144  
 Arg Ser Arg Val Arg Lys Thr Thr Glu Arg Ser Leu Ala Arg Val Arg  
 35 40 45  
 cga tcg acg agt gag aag gga agc gcg ctc gtg ctc gag cga gag agc 192  
 Arg Ser Thr Ser Glu Lys Gly Ser Ala Leu Val Leu Glu Arg Glu Ser  
 50 55 60  
 gaa cgg gag aag gag gag gga ggg aaa gcg cga gcg gag gga ttg cga 240  
 Glu Arg Glu Lys Glu Glu Gly Gly Lys Ala Arg Ala Glu Gly Leu Arg  
 65 70 75 80  
 ttc caa cgc ccg gac gtc gcc gcg ccg ggg gga gcg gat cct tgg aac 288  
 Phe Gln Arg Pro Asp Val Ala Ala Pro Gly Gly Ala Asp Pro Trp Asn  
 85 90 95  
 gac gag aag tgg aca aag acc aag tgg acg gta ttc aga gac gtc gcg 336  
 Asp Glu Lys Trp Thr Lys Thr Lys Trp Thr Val Phe Arg Asp Val Ala  
 100 105 110  
 tac gat ctc gat cct ttc ttc gct cga cac ccc gga gga gac tgg ctc 384  
 Tyr Asp Leu Asp Pro Phe Phe Ala Arg His Pro Gly Gly Asp Trp Leu  
 115 120 125  
 ctg aac ttg gcc gtg gga cga gac tgc acc gcg ctc atc gaa tcc tat 432  
 Leu Asn Leu Ala Val Gly Arg Asp Cys Thr Ala Leu Ile Glu Ser Tyr  
 130 135 140  
 cac ttg cga cca gag gtg gcg acg gct cgt ttc aga atg ctg ccc aaa 480  
 His Leu Arg Pro Glu Val Ala Thr Ala Arg Phe Arg Met Leu Pro Lys  
 145 150 155 160  
 ctc gag gat ttt ccc gtc gag gcc gtg ccc aag tcc ccg aga ccg aac 528  
 Leu Glu Asp Phe Pro Val Glu Ala Val Pro Lys Ser Pro Arg Pro Asn

148

165										170					175					
gat	tcg	ccg	tta	tac	aac	aac	att	cgc	aac	cga	gtc	cgc	gaa	gag	ctc	576				
Asp	Ser	Pro	Leu	Tyr	Asn	Asn	Ile	Arg	Asn	Arg	Val	Arg	Glu	Glu	Leu					
			180					185					190							
ttc	cca	gag	gag	gga	aag	aat	atg	cac	aga	cag	ggc	ggc	gac	cac	ggc	624				
Phe	Pro	Glu	Glu	Gly	Lys	Asn	Met	His	Arg	Gln	Gly	Gly	Asp	His	Gly					
		195					200					205								
gac	ggt	gac	gat	tct	ggg	ttt	cgc	cgc	ctt	ttg	ctt	atg	ccg	tgt	acc	672				
Asp	Gly	Asp	Asp	Ser	Gly	Phe	Arg	Arg	Leu	Leu	Leu	Met	Pro	Cys	Thr					
	210					215					220									
tat	tcc	ctt	ccg	ggg	gtt	cct	ttc	cgg	ctg	cct	cct	cgg	gtc	tcg	cgg	720				
Tyr	Ser	Leu	Pro	Gly	Val	Pro	Phe	Arg	Leu	Pro	Pro	Arg	Val	Ser	Arg					
225					230					235					240					
ggg	cgt	gga	ttg	gtc	tca	cga	ttc	agg	cac	tgc	gcc	aac	cac	ggc	gcg	768				
Gly	Arg	Gly	Leu	Val	Ser	Arg	Phe	Arg	His	Cys	Ala	Asn	His	Gly	Ala					
				245					250					255						
atg	tct	cct	tcg	ccg	gcc	gtt	aac	ggc	gtc	ctc	ggt	ttg	acg	aac	gat	816				
Met	Ser	Pro	Ser	Pro	Ala	Val	Asn	Gly	Val	Leu	Gly	Leu	Thr	Asn	Asp					
			260					265					270							
ctc	atc	ggc	ggc	tcg	tcc	ttg	atg	tgg	aga	tat	cac	cac	caa	gtc	agc	864				
Leu	Ile	Gly	Gly	Ser	Ser	Leu	Met	Trp	Arg	Tyr	His	His	Gln	Val	Ser					
		275					280					285								
cac	cac	att	cat	tgc	aac	gac	aac	gcc	atg	gat	caa	gac	gtg	tac	acg	912				
His	His	Ile	His	Cys	Asn	Asp	Asn	Ala	Met	Asp	Gln	Asp	Val	Tyr	Thr					
		290				295					300									
gcg	atg	cca	tta	ttg	cgt	ttc	gac	gct	cgc	cgg	ccc	aag	tcc	tgg	tac	960				
Ala	Met	Pro	Leu	Leu	Arg	Phe	Asp	Ala	Arg	Arg	Pro	Lys	Ser	Trp	Tyr					
305					310					315					320					
cat	cgc	ttc	cag	cag	tgg	tac	atg	ttt	tta	gcg	ttc	ccg	ttg	ttg	cag	1008				
His	Arg	Phe	Gln	Gln	Trp	Tyr	Met	Phe	Leu	Ala	Phe	Pro	Leu	Leu	Gln					
			325						330					335						
gtt	gcc	ttc	caa	gtc	gga	gac	att	gcc	gca	ctg	ttc	acg	cgt	gat	acc	1056				
Val	Ala	Phe	Gln	Val	Gly	Asp	Ile	Ala	Ala	Leu	Phe	Thr	Arg	Asp	Thr					
			340					345					350							
gaa	ggc	gct	aag	ctt	cac	ggg	gcg	acg	acg	tgg	gag	ctt	acc	acg	gtt	1104				
Glu	Gly	Ala	Lys	Leu	His	Gly	Ala	Thr	Thr	Trp	Glu	Leu	Thr	Thr	Val					
		355					360					365								
gtc	ctc	ggt	aag	att	gtg	cac	ttc	ggt	ctt	ttg	ttg	ggg	ccg	ttg	atg	1152				
Val	Leu	Gly	Lys	Ile	Val	His	Phe	Gly	Leu	Leu	Leu	Gly	Pro	Leu	Met					
		370			</															

149

435	440	445	
ata ggt aac ttc ttc acg ggt ggc ctc aac ttg	caa gtt gag cac cac	1392	
Ile Gly Asn Phe Phe Thr Gly Gly Leu Asn Leu	Gln Val Glu His His		
450	455 460		
ttg ttt ccg gcg att tgc ttc gtc cac tac ccg	gac atc gcg aag atc	1440	
Leu Phe Pro Ala Ile Cys Phe Val His Tyr Pro	Asp Ile Ala Lys Ile		
465	470 475 480		
gtg aag gaa gaa gcg gcc aag ctc aac atc cct	tac gcg tct tac agg	1488	
Val Lys Glu Glu Ala Ala Lys Leu Asn Ile Pro	Tyr Ala Ser Tyr Arg		
	485 490 495		
act ctt cct ggt att ttc gtc caa ttc tgg aga	ttt atg aag gac atg	1536	
Thr Leu Pro Gly Ile Phe Val Gln Phe Trp Arg	Phe Met Lys Asp Met		
	500 505 510		
ggc acg gct gag caa att ggt gaa gtt cca ttg	ccg aag att ccc aac	1584	
Gly Thr Ala Glu Gln Ile Gly Glu Val Pro Leu	Pro Lys Ile Pro Asn		
	515 520 525		
ccg cag ctc gcg ccg aag ctc gct tag		1611	
Pro Gln Leu Ala Pro Lys Leu Ala			
	530 535		

&lt;210&gt; 96

&lt;211&gt; 536

&lt;212&gt; PRT

<213> *Ostreococcus tauri*

&lt;400&gt; 96

Met Tyr Leu Gly Arg Gly Arg Leu Glu Ser Gly Thr Thr Arg Gly Met
1 5 10 15

Met Arg Thr His Ala Arg Arg Pro Ser Thr Thr Ser Asn Pro Cys Ala
20 25 30

Arg Ser Arg Val Arg Lys Thr Thr Glu Arg Ser Leu Ala Arg Val Arg
35 40 45

Arg Ser Thr Ser Glu Lys Gly Ser Ala Leu Val Leu Glu Arg Glu Ser
50 55 60

Glu Arg Glu Lys Glu Glu Gly Gly Lys Ala Arg Ala Glu Gly Leu Arg
65 70 75 80

Phe Gln Arg Pro Asp Val Ala Ala Pro Gly Gly Ala Asp Pro Trp Asn
85 90 95

Asp Glu Lys Trp Thr Lys Thr Lys Trp Thr Val Phe Arg Asp Val Ala
100 105 110

Tyr Asp Leu Asp Pro Phe Phe Ala Arg His Pro Gly Gly Asp Trp Leu
115 120 125

Leu Asn Leu Ala Val Gly Arg Asp Cys Thr Ala Leu Ile Glu Ser Tyr
130 135 140

His Leu Arg Pro Glu Val Ala Thr Ala Arg Phe Arg Met Leu Pro Lys  
145 150 155 160

Leu Glu Asp Phe Pro Val Glu Ala Val Pro Lys Ser Pro Arg Pro Asn  
165 170 175

Asp Ser Pro Leu Tyr Asn Asn Ile Arg Asn Arg Val Arg Glu Glu Leu  
180 185 190

Phe Pro Glu Glu Gly Lys Asn Met His Arg Gln Gly Gly Asp His Gly  
195 200 205

Asp Gly Asp Asp Ser Gly Phe Arg Arg Leu Leu Leu Met Pro Cys Thr  
210 215 220

Tyr Ser Leu Pro Gly Val Pro Phe Arg Leu Pro Pro Arg Val Ser Arg  
225 230 235 240

Gly Arg Gly Leu Val Ser Arg Phe Arg His Cys Ala Asn His Gly Ala  
245 250 255

Met Ser Pro Ser Pro Ala Val Asn Gly Val Leu Gly Leu Thr Asn Asp  
260 265 270

Leu Ile Gly Gly Ser Ser Leu Met Trp Arg Tyr His His Gln Val Ser  
275 280 285

His His Ile His Cys Asn Asp Asn Ala Met Asp Gln Asp Val Tyr Thr  
290 295 300

Ala Met Pro Leu Leu Arg Phe Asp Ala Arg Arg Pro Lys Ser Trp Tyr  
305 310 315 320

His Arg Phe Gln Gln Trp Tyr Met Phe Leu Ala Phe Pro Leu Leu Gln  
325 330 335

Val Ala Phe Gln Val Gly Asp Ile Ala Ala Leu Phe Thr Arg Asp Thr  
340 345 350

Glu Gly Ala Lys Leu His Gly Ala Thr Thr Trp Glu Leu Thr Thr Val  
355 360 365

Val Leu Gly Lys Ile Val His Phe Gly Leu Leu Leu Gly Pro Leu Met  
370 375 380

Asn His Ala Val Ser Ser Val Leu Leu Gly Ile Val Gly Phe Met Ala  
385 390 395 400

Cys Gln Gly Ile Val Leu Ala Cys Thr Phe Ala Val Ser His Asn Val  
405 410 415

Ala Glu Ala Lys Ile Pro Glu Asp Thr Gly Gly Glu Ala Trp Glu Arg  
420 425 430

Asp Trp Gly Val Gln Gln Leu Val Thr Ser Ala Asp Trp Gly Gly Lys  
435 440 445

Ile Gly Asn Phe Phe Thr Gly Gly Leu Asn Leu Gln Val Glu His His  
450 455 460

Leu Phe Pro Ala Ile Cys Phe Val His Tyr Pro Asp Ile Ala Lys Ile  
465 470 475 480

Val Lys Glu Glu Ala Ala Lys Leu Asn Ile Pro Tyr Ala Ser Tyr Arg  
485 490 495

Thr Leu Pro Gly Ile Phe Val Gln Phe Trp Arg Phe Met Lys Asp Met  
500 505 510

Gly Thr Ala Glu Gln Ile Gly Glu Val Pro Leu Pro Lys Ile Pro Asn  
515 520 525

Pro Gln Leu Ala Pro Lys Leu Ala  
530 535

<210> 97  
<211> 1455  
<212> DNA  
<213> *Thalassiosira pseudonana*

<220>  
<221> CDS  
<222> (1)..(1455)  
<223> Delta-6-Desaturase

<400> 97  
.atg gga aaa gga gga gac gca gcc gca gct acc aag cgt agt gga gca 48  
Met Gly Lys Gly Gly Asp Ala Ala Ala Thr Lys Arg Ser Gly Ala  
1 5 10 15  
ttg aaa ttg gcg gag aag ccg cag aag tac act tgg cag gag gtg aag 96  
Leu Lys Leu Ala Glu Lys Pro Gln Lys Tyr Thr Trp Gln Glu Val Lys  
20 25 30  
aag cac atc acc ccc gac gat gcc tgg gta gtc cac caa aac aaa gtc 144  
Lys His Ile Thr Pro Asp Asp Ala Trp Val Val His Gln Asn Lys Val  
35 40 45  
tac gac gtc tcc aac tgg tac gac cac ccc ggt gga gcc gtg gtg ttc 192  
Tyr Asp Val Ser Asn Trp Tyr Asp His Pro Gly Gly Ala Val Val Phe  
50 55 60  
acc cac gcc gga gac gac atg acg gac atc ttc gcc gcc ttc cac gcc 240  
Thr His Ala Gly Asp Asp Met Thr Asp Ile Phe Ala Ala Phe His Ala  
65 70 75 80  
caa ggc tct cag gcc atg atg aag aag ttt tac att gga gat ttg att 288  
Gln Gly Ser Gln Ala Met Met Lys Lys Phe Tyr Ile Gly Asp Leu Ile

95

ccg	gag	agt	gtg	gag	cat	aag	gat	caa	aga	cag	ttg	gat	ttc	gag	aag	336
Pro	Glu	Ser	Val	Glu	His	Lys	Asp	Gln	Arg	Gln	Leu	Asp	Phe	Glu	Lys	
			100					105					110			
gga	tat	cgt	gat	tta	cgg	gcc	aag	ctt	gtc	atg	atg	ggg	atg	ttc	aag	384
Gly	Tyr	Arg	Asp	Leu	Arg	Ala	Lys	Leu	Val	Met	Met	Gly	Met	Phe	Lys	
		115					120					125				
tcg	agt	aag	atg	tat	tat	gca	tac	aag	tgc	tcg	ttc	aat	atg	tgc	atg	432
Ser	Ser	Lys	Met	Tyr	Tyr	Ala	Tyr	Lys	Cys	Ser	Phe	Asn	Met	Cys	Met	
		130				135					140					
tgg	ttg	gtg	gcg	gtg	gcc	atg	gtg	tac	tac	tcg	gac	agt	ttg	gca	atg	480
Trp	Leu	Val	Ala	Val	Ala	Met	Val	Tyr	Tyr	Ser	Asp	Ser	Leu	Ala	Met	
145					150					155					160	
cac	att	gga	tcg	gct	ctc	ttg	ttg	gga	ttg	ttc	tgg	cag	cag	tgt	gga	528
His	Ile	Gly	Ser	Ala	Leu	Leu	Leu	Gly	Leu	Phe	Trp	Gln	Gln	Cys	Gly	
				165					170					175		
tgg	ctt	gcg	cac	gac	ttt	ctt	cac	cac	caa	gtc	ttt	aag	caa	cga	aag	576
Trp	Leu	Ala	His	Asp	Phe	Leu	His	His	Gln	Val	Phe	Lys	Gln	Arg	Lys	
			180					185					190			
tac	gga	gat	ctc	gtt	ggc	atc	ttt	tgg	gga	gat	ctc	atg	cag	ggg	ttc	624
Tyr	Gly	Asp	Leu	Val	Gly	Ile	Phe	Trp	Gly	Asp	Leu	Met	Gln	Gly	Phe	
		195					200					205				
tcg	atg	cag	tgg	tgg	aag	aac	aag	cac	aat	ggc	cac	cat	gct	gtt	ccc	672
Ser	Met	Gln	Trp	Trp	Lys	Asn	Lys	His	Asn	Gly	His	His	Ala	Val	Pro	
		210				215					220					
aac	ttg	cac	aac	tct	tcc	ttg	gac	agt	cag	gat	ggt	gat	ccc	gat	att	720
Asn	Leu	His	Asn	Ser	Ser	Leu	Asp	Ser	Gln	Asp	Gly	Asp	Pro	Asp	Ile	
225					230					235					240	
gat	acc	atg	cca	ctc	ctt	gct	tgg	agt	ctc	aag	cag	gct	cag	agt	ttc	768
Asp	Thr	Met	Pro	Leu	Leu	Ala	Trp	Ser	Leu	Lys	Gln	Ala	Gln	Ser	Phe	
				245					250					255		
aga	gag	atc	aat	aag	gga	aag	gac	agt	acc	ttc	gtc	aag	tac	gct	atc	816
Arg	Glu	Ile	Asn	Lys	Gly	Lys	Asp	Ser	Thr	Phe	Val	Lys	Tyr	Ala	Ile	
			260					265					270			
aaa	ttc	cag	gca	ttc	aca	tac	ttc	ccc	atc	ctc	ctc	ttg	gct	cgc	atc	864
Lys	Phe	Gln	Ala	Phe	Thr	Tyr	Phe	Pro	Ile	Leu	Leu	Leu	Ala	Arg	Ile	
		275					280					285				
tct	tgg	ttg	aat	gaa	tcc	ttc	aaa	act	gca	ttc	gga	ctc	gga	gct	gcc	912
Ser	Trp	Leu	Asn	Glu	Ser	Phe	Lys	Thr	Ala	Phe	Gly	Leu	Gly	Ala	Ala	
		290				295					300					



153

355	360	365	
gga ttg gga cac aac ggt atg tca gtg tac gat gcc acc acc cga cct			1152
Gly Leu Gly His Asn Gly Met Ser Val Tyr Asp Ala Thr Thr Arg Pro			
370	375	380	
gac ttc tgg caa ctc caa gtc acc act aca cgt aac atc att ggt gga			1200
Asp Phe Trp Gln Leu Gln Val Thr Thr Thr Arg Asn Ile Ile Gly Gly			
385	390	395	400
cac ggc att ccc caa ttc ttt gtg gat tgg ttc tgc ggt gga ttg caa			1248
His Gly Ile Pro Phe Phe Val Asp Trp Phe Cys Gly Gly Leu Gln			
405	410		415
tac caa gtg gat cac cac ctc ttc ccc atg atg cct aga aac aat atc			1296
Tyr Gln Val Asp His His Leu Phe Pro Met Met Pro Arg Asn Asn Ile			
420	425		430
gcg aaa tgc cac aag ctt gtg gag tca ttc tgt aag gag tgg ggt gtg			1344
Ala Lys Cys His Lys Leu Val Glu Ser Phe Cys Lys Glu Trp Gly Val			
435	440		445
aag tac cat gag gcc gat atg tgg gat ggt acc gtg gaa gtg ttg caa			1392
Lys Tyr His Glu Ala Asp Met Trp Asp Gly Thr Val Glu Val Leu Gln			
450	455		460
cat ctc tcc aag gtg tcg gat gat ttc ctt gtg gag atg gtg aag gat			1440
His Leu Ser Lys Val Ser Asp Asp Phe Leu Val Glu Met Val Lys Asp			
465	470	475	480
ttc cct gcc atg taa			1455
Phe Pro Ala Met			

&lt;210&gt; 98

&lt;211&gt; 484

&lt;212&gt; PRT

&lt;213&gt; Thalassiosira pseudonana

&lt;400&gt; 98

Met Gly Lys Gly Gly Asp Ala Ala Ala Ala Thr Lys Arg Ser Gly Ala
1 5 10 15

Leu Lys Leu Ala Glu Lys Pro Gln Lys Tyr Thr Trp Gln Glu Val Lys
20 25 30

Lys His Ile Thr Pro Asp Asp Ala Trp Val Val His Gln Asn Lys Val
35 40 45

Tyr Asp Val Ser Asn Trp Tyr Asp His Pro Gly Gly Ala Val Val Phe
50 55 60

Thr His Ala Gly Asp Asp Met Thr Asp Ile Phe Ala Ala Phe His Ala
65 70 75 80

Gln Gly Ser Gln Ala Met Met Lys Lys Phe Tyr Ile Gly Asp Leu Ile
85 90 95

Pro Glu Ser Val Glu His Lys Asp Gln Arg Gln Leu Asp Phe Glu Lys
100 105 110

Gly Tyr Arg Asp Leu Arg Ala Lys Leu Val Met Met Gly Met Phe Lys  
 115 120 125

Ser Ser Lys Met Tyr Tyr Ala Tyr Lys Cys Ser Phe Asn Met Cys Met  
 130 135 140

Trp Leu Val Ala Val Ala Met Val Tyr Tyr Ser Asp Ser Leu Ala Met  
 145 150 155 160

His Ile Gly Ser Ala Leu Leu Leu Gly Leu Phe Trp Gln Gln Cys Gly  
 165 170 175

Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Lys Gln Arg Lys  
 180 185 190

Tyr Gly Asp Leu Val Gly Ile Phe Trp Gly Asp Leu Met Gln Gly Phe  
 195 200 205

Ser Met Gln Trp Trp Lys Asn Lys His Asn Gly His His Ala Val Pro  
 210 215 220

Asn Leu His Asn Ser Ser Leu Asp Ser Gln Asp Gly Asp Pro Asp Ile  
 225 230 235 240

Asp Thr Met Pro Leu Leu Ala Trp Ser Leu Lys Gln Ala Gln Ser Phe  
 245 250 255

Arg Glu Ile Asn Lys Gly Lys Asp Ser Thr Phe Val Lys Tyr Ala Ile  
 260 265 270

Lys Phe Gln Ala Phe Thr Tyr Phe Pro Ile Leu Leu Leu Ala Arg Ile  
 275 280 285

Ser Trp Leu Asn Glu Ser Phe Lys Thr Ala Phe Gly Leu Gly Ala Ala  
 290 295 300

Ser Glu Asn Ala Lys Leu Glu Leu Glu Lys Arg Gly Leu Gln Tyr Pro  
 305 310 315 320

Leu Leu Glu Lys Leu Gly Ile Thr Leu His Tyr Thr Trp Met Phe Val  
 325 330 335

Leu Ser Ser Gly Phe Gly Arg Trp Ser Leu Pro Tyr Ser Ile Met Tyr  
 340 345 350

Phe Phe Thr Ala Thr Cys Ser Ser Gly Leu Phe Leu Ala Leu Val Phe  
 355 360 365

Gly Leu Gly His Asn Gly Met Ser Val Tyr Asp Ala Thr Thr Arg Pro  
 370 375 380

Asp Phe Trp Gln Leu Gln Val Thr Thr Thr Arg Asn Ile Ile Gly Gly  
385 390 395 400

His Gly Ile Pro Gln Phe Phe Val Asp Trp Phe Cys Gly Gly Leu Gln  
405 410 415

Tyr Gln Val Asp His His Leu Phe Pro Met Met Pro Arg Asn Asn Ile  
420 425 430

Ala Lys Cys His Lys Leu Val Glu Ser Phe Cys Lys Glu Trp Gly Val  
435 440 445

Lys Tyr His Glu Ala Asp Met Trp Asp Gly Thr Val Glu Val Leu Gln  
450 455 460

His Leu Ser Lys Val Ser Asp Asp Phe Leu Val Glu Met Val Lys Asp  
465 470 475 480

Phe Pro Ala Met

<210> 99  
<211> 1431  
<212> DNA  
<213> *Thalassiosira pseudonana*  
  
<220>  
<221> CDS  
<222> (1)..(1431)  
<223> Delta-5-Desaturase

<400> 99  
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Met Pro Pro Asn Ala Asp Ile Ser Arg Ile Arg Asn Arg Ile Pro Thr  
1 5 10 15  
  
aaa aca ggt acc gtt gcc tct gcc gac aac aac gac ccc gcc acc caa 96  
Lys Thr Gly Thr Val Ala Ser Ala Asp Asn Asn Asp Pro Ala Thr Gln  
20 25 30  
  
tcc gtc cga acc ctc aaa tct ctc aag ggc aac gag gtc gtc atc aac 144  
Ser Val Arg Thr Leu Lys Ser Leu Lys Gly Asn Glu Val Val Ile Asn  
35 40 45  
  
ggc aca att tat gac att gct gac ttt gtc cat cct gga gga gag gtt 192  
Gly Thr Ile Tyr Asp Ile Ala Asp Phe Val His Pro Gly Gly Glu Val  
50 55 60  
  
gtc aag ttc ttt ggt ggg aat gat gtt act att cag tat aat atg att 240  
Val Lys Phe Phe Gly Gly Asn Asp Val Thr Ile Gln Tyr Asn Met Ile  
65 70 75 80  
  
cat ccg tat cat acg ggg aaa cat ctg gag aag atg aag gct gtt gga 288  
His Pro Tyr His Thr Gly Lys His Leu Glu Lys Met Lys Ala Val Gly  
85 90 95  
  
aag gtt gta gat tgg cag tcg gac tac aag ttc gac acc ccc ttt gaa 336  
Lys Val Val Asp Trp Gln Ser Asp Tyr Lys Phe Asp Thr Pro Phe Glu

## 156

100	105	110	
cga gag atc aaa tca gaa gtg ttc aag atc gta cgt cgc ggg cgt gag Arg Glu Ile Lys Ser Glu Val Phe Lys Ile Val Arg Arg Gly Arg Glu 115 120 125			384
ttc ggc aca aca ggc tac ttc ctc cgt gcc ttt ttc tac atc gct ctc Phe Gly Thr Thr Gly Tyr Phe Leu Arg Ala Phe Phe Tyr Ile Ala Leu 130 135 140			432
ttc ttc acc atg caa tac act ttc gcc aca tgc acc acc ttc acc acc Phe Phe Thr Met Gln Tyr Thr Phe Ala Thr Cys Thr Thr Phe Thr Thr 145 150 155 160			480
tac gat cac tgg tat cag agt ggt gta ttc atc gca att gtg ttt ggt Tyr Asp His Trp Tyr Gln Ser Gly Val Phe Ile Ala Ile Val Phe Gly 165 170 175			528
att tca cag gca ttc att ggg ttg aat gtc cag cac gat gcc aat cac Ile Ser Gln Ala Phe Ile Gly Leu Asn Val Gln His Asp Ala Asn His 180 185 190			576
gga gct gcc agt aag cgt ccc tgg gtg aat gac ttg ttg gga ttt gga Gly Ala Ala Ser Lys Arg Pro Trp Val Asn Asp Leu Leu Gly Phe Gly 195 200 205			624
acg gat ttg att gga tct aac aaa tgg aat tgg atg gca cag cat tgg Thr Asp Leu Ile Gly Ser Asn Lys Trp Asn Trp Met Ala Gln His Trp 210 215 220			672
act cat cac gct tac act aac cat agt gag aag gat ccc gat agc ttc Thr His His Ala Tyr Thr Asn His Ser Glu Lys Asp Pro Asp Ser Phe 225 230 235 240			720
agc tcg gaa cct atg ttt gca ttc aat gac tat ccc att gga cac ccg Ser Ser Glu Pro Met Phe Ala Phe Asn Asp Tyr Pro Ile Gly His Pro 245 250 255			768
aag aga aag tgg tgg cat agg ttc cag gga ggg tac ttc ctc ttc atg Lys Arg Lys Trp Trp His Arg Phe Gln Gly Gly Tyr Phe Leu Phe Met 260 265 270			816
ctt gga ctt tac tgg ctc tcg act gta ttc aat ccg caa ttc att gat Leu Gly Leu Tyr Trp Leu Ser Thr Val Phe Asn Pro Gln Phe Ile Asp 275 280 285			864
ctt cgt caa cgt ggg gct cag tac gtc gga att caa atg gag aat gat Leu Arg Gln Arg Gly Ala Gln Tyr Val Gly Ile Gln Met Glu Asn Asp 290 295 300			912
ttc att gtc aag agg agg aag tac gcc gtt gca ttg agg atg atg tac Phe Ile Val Lys Arg Arg Lys Tyr Ala Val Ala Leu Arg Met Met Tyr 305 310 315 320			960
att tac ttg aac att gtc agc ccc ttc atg aac aat ggt ttg agc tgg Ile Tyr Leu Asn Ile Val Ser Pro Phe Met Asn Asn Gly Leu Ser Trp 325 330 335			1008
tct acc ttt gga atc atc atg ttg atg gga atc agc gag agt ctc act Ser Thr Phe Gly Ile Ile Met Leu Met Gly Ile Ser Glu Ser Leu Thr 340 345 350			1056
ctc agt gtg ctc ttc tcg ttg tct cac aac ttc atc aat tcg gat cgt Leu Ser Val Leu Phe Ser Leu Ser His Asn Phe Ile Asn Ser Asp Arg 355 360 365			1104
gat cct acg gct gac ttc aaa aag acc gga gaa caa gtg tgc tgg ttc Asp Pro Thr Ala Asp Phe Lys Lys Thr Gly Glu Gln Val Cys Trp Phe			1152

370 375 380  
 aag tcg cag gtg gag act tcg tct acc tat ggg ggt ttt att tcc gga 1200  
 Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr Gly Gly Phe Ile Ser Gly  
 385 390 395 400  
 tgt ctt acg gga gga ctc aac ttt cag gtg gaa cat cat ctc ttt ccc 1248  
 Cys Leu Thr Gly Gly Leu Asn Phe Gln Val Glu His His Leu Phe Pro  
 405 410 415  
 cgt atg agc agt gct tgg tat cct tac att gca cct acg gtt cgt gag 1296  
 Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala Pro Thr Val Arg Glu  
 420 425 430  
 gtt tgc aag aag cac ggg gtg aac tac gct tat tat cct tgg att ggg 1344  
 Val Cys Lys Lys His Gly Val Asn Tyr Ala Tyr Tyr Pro Trp Ile Gly  
 435 440 445  
 cag aat ttg gta tca aca ttc aaa tac atg cat cgc gct ggt agt gga 1392  
 Gln Asn Leu Val Ser Thr Phe Lys Tyr Met His Arg Ala Gly Ser Gly  
 450 455 460  
 gcc aac tgg gag ctc aag ccg ttg tct gga agt gcc taa 1431  
 Ala Asn Trp Glu Leu Lys Pro Leu Ser Gly Ser Ala  
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 <213> *Thalassiosira pseudonana*  
  
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 Lys Thr Gly Thr Val Ala Ser Ala Asp Asn Asn Asp Pro Ala Thr Gln  
 20 25 30  
 Ser Val Arg Thr Leu Lys Ser Leu Lys Gly Asn Glu Val Val Ile Asn  
 35 40 45  
 Gly Thr Ile Tyr Asp Ile Ala Asp Phe Val His Pro Gly Gly Glu Val  
 50 55 60  
 Val Lys Phe Phe Gly Gly Asn Asp Val Thr Ile Gln Tyr Asn Met Ile  
 65 70 75 80  
 His Pro Tyr His Thr Gly Lys His Leu Glu Lys Met Lys Ala Val Gly  
 85 90 95  
 Lys Val Val Asp Trp Gln Ser Asp Tyr Lys Phe Asp Thr Pro Phe Glu  
 100 105 110  
 Arg Glu Ile Lys Ser Glu Val Phe Lys Ile Val Arg Arg Gly Arg Glu  
 115 120 125  
 Phe Gly Thr Thr Gly Tyr Phe Leu Arg Ala Phe Phe Tyr Ile Ala Leu  
 130 135 140

Phe Phe Thr Met Gln Tyr Thr Phe Ala Thr Cys Thr Thr Phe Thr Thr  
 145 150 155 160

Tyr Asp His Trp Tyr Gln Ser Gly Val Phe Ile Ala Ile Val Phe Gly  
 165 170 175

Ile Ser Gln Ala Phe Ile Gly Leu Asn Val Gln His Asp Ala Asn His  
 180 185 190

Gly Ala Ala Ser Lys Arg Pro Trp Val Asn Asp Leu Leu Gly Phe Gly  
 195 200 205

Thr Asp Leu Ile Gly Ser Asn Lys Trp Asn Trp Met Ala Gln His Trp  
 210 215 220

Thr His His Ala Tyr Thr Asn His Ser Glu Lys Asp Pro Asp Ser Phe  
 225 230 235 240

Ser Ser Glu Pro Met Phe Ala Phe Asn Asp Tyr Pro Ile Gly His Pro  
 245 250 255

Lys Arg Lys Trp Trp His Arg Phe Gln Gly Gly Tyr Phe Leu Phe Met  
 260 265 270

Leu Gly Leu Tyr Trp Leu Ser Thr Val Phe Asn Pro Gln Phe Ile Asp  
 275 280 285

Leu Arg Gln Arg Gly Ala Gln Tyr Val Gly Ile Gln Met Glu Asn Asp  
 290 295 300

Phe Ile Val Lys Arg Arg Lys Tyr Ala Val Ala Leu Arg Met Met Tyr  
 305 310 315 320

Ile Tyr Leu Asn Ile Val Ser Pro Phe Met Asn Asn Gly Leu Ser Trp  
 325 330 335

Ser Thr Phe Gly Ile Ile Met Leu Met Gly Ile Ser Glu Ser Leu Thr  
 340 345 350

Leu Ser Val Leu Phe Ser Leu Ser His Asn Phe Ile Asn Ser Asp Arg  
 355 360 365

Asp Pro Thr Ala Asp Phe Lys Lys Thr Gly Glu Gln Val Cys Trp Phe  
 370 375 380

Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr Gly Gly Phe Ile Ser Gly  
 385 390 395 400

Cys Leu Thr Gly Gly Leu Asn Phe Gln Val Glu His His Leu Phe Pro  
 405 410 415

Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala Pro Thr Val Arg Glu  
420 425 430

Val Cys Lys Lys His Gly Val Asn Tyr Ala Tyr Tyr Pro Trp Ile Gly  
435 440 445

Gln Asn Leu Val Ser Thr Phe Lys Tyr Met His Arg Ala Gly Ser Gly  
450 455 460

Ala Asn Trp Glu Leu Lys Pro Leu Ser Gly Ser Ala  
465 470 475

<210> 101

<211> 1449

<212> DNA

<213> *Thalassiosira pseudonana*

<220>

<221> CDS

<222> (1)..(1449)

<223> Delta-5-Desaturase

<400> 101

atg cca ccc aac gcc gag gtc aaa aac ctc cgt tca cgt tcc atc cca 48  
Met Pro Pro Asn Ala Glu Val Lys Asn Leu Arg Ser Arg Ser Ile Pro  
1 5 10 15

acg aag aag tcc agt tca tcg tca tcc acc gcg aac gac gat ccg gct 96  
Thr Lys Lys Ser Ser Ser Ser Ser Ser Thr Ala Asn Asp Asp Pro Ala  
20 25 30

acc caa tcc acc tca cct gtg aac cga acc ctc aag tct ttg aat gga 144  
Thr Gln Ser Thr Ser Pro Val Asn Arg Thr Leu Lys Ser Leu Asn Gly  
35 40 45

aac gaa ata gct att gac ggt gtc atc tat gat att gat ggc ttt gtc 192  
Asn Glu Ile Ala Ile Asp Gly Val Ile Tyr Asp Ile Asp Gly Phe Val  
50 55 60

cat cct gga gga gag gtt att agc ttc ttt gga ggc aac gat gtg act 240  
His Pro Gly Gly Glu Val Ile Ser Phe Phe Gly Gly Asn Asp Val Thr  
65 70 75 80

gta cag tac aaa atg att cat ccg tat cat aat agt aag cat ctc gag 288  
Val Gln Tyr Lys Met Ile His Pro Tyr His Asn Ser Lys His Leu Glu  
85 90 95

aag atg aga gcc gtt gga aag att gca gac tac tcc aca gag tac aag 336  
Lys Met Arg Ala Val Gly Lys Ile Ala Asp Tyr Ser Thr Glu Tyr Lys  
100 105 110

ttc gac aca ccc ttt gaa cga gag atc aaa tcc gaa gtg ttc aaa atc 384  
Phe Asp Thr Pro Phe Glu Arg Glu Ile Lys Ser Glu Val Phe Lys Ile  
115 120 125

gtc cgt cga gga cgt gaa ttc ggt aca aca gga tat ttc ctc cgt gcc 432  
Val Arg Arg Gly Arg Glu Phe Gly Thr Thr Gly Tyr Phe Leu Arg Ala  
130 135 140

ttc ttc tac att gct ctc ttc ttc acc atg caa tac acc ttc gcc aca 480  
Phe Phe Tyr Ile Ala Leu Phe Phe Thr Met Gln Tyr Thr Phe Ala Thr

## 160

145	150	155	160	
tgc act acc ttc acc acc tac gat cat tgg tat caa agt ggt gta ttc Cys Thr Thr Phe Thr Tyr Asp His Trp Tyr Gln Ser Gly Val Phe 165 170 175				528
atc gcc att gtg ttt ggt atc tca caa gct ttc att ggg ttg aat gta Ile Ala Ile Val Phe Gly Ile Ser Gln Ala Phe Ile Gly Leu Asn Val 180 185 190				576
caa cat gat gcc aat cac gga gct gct agc aaa cga cct tgg gtg aat Gln His Asp Ala Asn His Gly Ala Ala Ser Lys Arg Pro Trp Val Asn 195 200 205				624
gat ctc ctt gga tct gga gct gat ctc atc ggt gga tgc aaa tgg aac Asp Leu Leu Gly Ser Gly Ala Asp Leu Ile Gly Gly Cys Lys Trp Asn 210 215 220				672
tgg ttg gct cag cat tgg act cat cat gcg tat acc aat cac gct gat Trp Leu Ala Gln His Trp Thr His His Ala Tyr Thr Asn His Ala Asp 225 230 235 240				720
aaa gat cct gat agc ttt agt tcc gag ccg gtc ttc aac ttt aac gat Lys Asp Pro Asp Ser Phe Ser Ser Glu Pro Val Phe Asn Phe Asn Asp 245 250 255				768
tat ccc att ggt cac ccc aaa aga aag tgg tgg cat agg ttc caa ggg Tyr Pro Ile Gly His Pro Lys Arg Lys Trp Trp His Arg Phe Gln Gly 260 265 270				816
ctc tac ttc cta atc atg ctg agt ttc tat tgg gta tcg atg gta ttc Leu Tyr Phe Leu Ile Met Leu Ser Phe Tyr Trp Val Ser Met Val Phe 275 280 285				864
aac cca caa gtt atc gac ctc cgt cat gct gga gct gcc tac gtt gga Asn Pro Gln Val Ile Asp Leu Arg His Ala Gly Ala Ala Tyr Val Gly 290 295 300				912
ttt cag atg gag aac gac ttt atc gtc aaa cgg aga aag tat gca atg Phe Gln Met Glu Asn Asp Phe Ile Val Lys Arg Arg Lys Tyr Ala Met 305 310 315 320				960
gca ctt cgt gca atg tac ttc tat ttc aac atc tat tgt ccg att gtc Ala Leu Arg Ala Met Tyr Phe Tyr Phe Asn Ile Tyr Cys Pro Ile Val 325 330 335				1008
aac aat gga ttg act tgg tcg aca gtt gga atc atc ctc tta atg gga Asn Asn Gly Leu Thr Trp Ser Thr Val Gly Ile Ile Leu Leu Met Gly 340 345 350				1056
gtt agc gaa agc ttc atg ctc tcc ggt cta ttc gta ctc tca cac aac Val Ser Glu Ser Phe Met Leu Ser Gly Leu Phe Val Leu Ser His Asn 355 360 365				1104
ttt gaa aat tcc gaa cgt gat cct acc tct gag tat cgc aag act ggt Phe Glu Asn Ser Glu Arg Asp Pro Thr Ser Glu Tyr Arg Lys Thr Gly 370 375 380				1152
gag caa gta tgt tgg ttc aag tct caa gtg gag act tct tct acc tac Glu Gln Val Cys Trp Phe Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr 385 390 395 400				1200
gga ggt atc gtt gct ggg tgt ctc act ggt gga ctc aac ttt caa gtg Gly Gly Ile Val Ala Gly Cys Leu Thr Gly Gly Leu Asn Phe Gln Val 405 410 415				1248
gag cat cat ttg ttc ccg agg atg agc agt gct tgg tat cct ttc atc Glu His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Phe Ile				1296



161

420	425	430	
gcg ccg aag gtt aga gag att tgt aag aag cat gga gtt aga tac gct			1344
Ala Pro Lys Val Arg Glu Ile Cys Lys Lys His Gly Val Arg Tyr Ala			
435	440	445	
tac tat ccg tac atc tgg cag aac ttg cat tct acc gtg agt tac atg			1392
Tyr Tyr Pro Tyr Ile Trp Gln Asn Leu His Ser Thr Val Ser Tyr Met			
450	455	460	
cat ggg acg gga acg gga gct aga tgg gag ctt cag ccg ttg tct gga			1440
His Gly Thr Gly Thr Gly Ala Arg Trp Glu Leu Gln Pro Leu Ser Gly			
465	470	475	480
agg gcg tag			1449
Arg Ala			

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 <211> 482  
 <212> PRT  
 <213> *Thalassiosira pseudonana*

<400> 102

Met Pro Pro Asn Ala Glu Val Lys Asn Leu Arg Ser Arg Ser Ile Pro			
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Thr Lys Lys Ser Ser Ser Ser Ser Ser Thr Ala Asn Asp Asp Pro Ala			
	20	25	30
Thr Gln Ser Thr Ser Pro Val Asn Arg Thr Leu Lys Ser Leu Asn Gly			
	35	40	45
Asn Glu Ile Ala Ile Asp Gly Val Ile Tyr Asp Ile Asp Gly Phe Val			
	50	55	60
His Pro Gly Gly Glu Val Ile Ser Phe Phe Gly Gly Asn Asp Val Thr			
	65	70	75
Val Gln Tyr Lys Met Ile His Pro Tyr His Asn Ser Lys His Leu Glu			
	85	90	95
Lys Met Arg Ala Val Gly Lys Ile Ala Asp Tyr Ser Thr Glu Tyr Lys			
	100	105	110
Phe Asp Thr Pro Phe Glu Arg Glu Ile Lys Ser Glu Val Phe Lys Ile			
	115	120	125
Val Arg Arg Gly Arg Glu Phe Gly Thr Thr Gly Tyr Phe Leu Arg Ala			
	130	135	140
Phe Phe Tyr Ile Ala Leu Phe Phe Thr Met Gln Tyr Thr Phe Ala Thr			
	145	150	155
Cys Thr Thr Phe Thr Thr Tyr Asp His Trp Tyr Gln Ser Gly Val Phe			
	165	170	175

Ile Ala Ile Val Phe Gly Ile Ser Gln Ala Phe Ile Gly Leu Asn Val  
 180 185 190

Gln His Asp Ala Asn His Gly Ala Ala Ser Lys Arg Pro Trp Val Asn  
 195 200 205

Asp Leu Leu Gly Ser Gly Ala Asp Leu Ile Gly Gly Cys Lys Trp Asn  
 210 215 220

Trp Leu Ala Gln His Trp Thr His His Ala Tyr Thr Asn His Ala Asp  
 225 230 235 240

Lys Asp Pro Asp Ser Phe Ser Ser Glu Pro Val Phe Asn Phe Asn Asp  
 245 250 255

Tyr Pro Ile Gly His Pro Lys Arg Lys Trp Trp His Arg Phe Gln Gly  
 260 265 270

Leu Tyr Phe Leu Ile Met Leu Ser Phe Tyr Trp Val Ser Met Val Phe  
 275 280 285

Asn Pro Gln Val Ile Asp Leu Arg His Ala Gly Ala Ala Tyr Val Gly  
 290 295 300

Phe Gln Met Glu Asn Asp Phe Ile Val Lys Arg Arg Lys Tyr Ala Met  
 305 310 315 320

Ala Leu Arg Ala Met Tyr Phe Tyr Phe Asn Ile Tyr Cys Pro Ile Val  
 325 330 335

Asn Asn Gly Leu Thr Trp Ser Thr Val Gly Ile Ile Leu Leu Met Gly  
 340 345 350

Val Ser Glu Ser Phe Met Leu Ser Gly Leu Phe Val Leu Ser His Asn  
 355 360 365

Phe Glu Asn Ser Glu Arg Asp Pro Thr Ser Glu Tyr Arg Lys Thr Gly  
 370 375 380

Glu Gln Val Cys Trp Phe Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr  
 385 390 395 400

Gly Gly Ile Val Ala Gly Cys Leu Thr Gly Gly Leu Asn Phe Gln Val  
 405 410 415

Glu His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Phe Ile  
 420 425 430

Ala Pro Lys Val Arg Glu Ile Cys Lys Lys His Gly Val Arg Tyr Ala  
 435 440 445

Tyr Tyr Pro Tyr Ile Trp Gln Asn Leu His Ser Thr Val Ser Tyr Met  
450 455 460

His Gly Thr Gly Thr Gly Ala Arg Trp Glu Leu Gln Pro Leu Ser Gly  
465 470 475 480

Arg Ala

<210> 103  
<211> 1512  
<212> DNA  
<213> *Thalassiosira pseudonana*

<220>  
<221> CDS  
<222> (1)..(1512)  
<223> Delta-4-Desaturase

<400> 103  
atg tgc aac ggc aac ctc cca gca tcc acc gca cag ctc aag tcc acc 48  
Met Cys Asn Gly Asn Leu Pro Ala Ser Thr Ala Gln Leu Lys Ser Thr  
1 5 10 15  
tcg aag ccc cag cag caa cat gag cat cgc acc atc tcc aag tcc gag 96  
Ser Lys Pro Gln Gln Gln His Glu His Arg Thr Ile Ser Lys Ser Glu  
20 25 30  
ctc gcc caa cac aac acg ccc aaa tca gca tgg tgt gcc gtc cac tcc 144  
Leu Ala Gln His Asn Thr Pro Lys Ser Ala Trp Cys Ala Val His Ser  
35 40 45  
act ccc gcc acc gac cca tcc cac tcc aac aac aaa caa cac gca cac 192  
Thr Pro Ala Thr Asp Pro Ser His Ser Asn Asn Lys Gln His Ala His  
50 55 60  
cta gtc ctc gac att acc gac ttt gcg tcc cgc cat cca ggg gga gac 240  
Leu Val Leu Asp Ile Thr Asp Phe Ala Ser Arg His Pro Gly Gly Asp  
65 70 75 80  
ctc atc ctc ctc gct tcc ggc aaa gac gcc tcg gtg ctg ttt gaa aca 288  
Leu Ile Leu Leu Ala Ser Gly Lys Asp Ala Ser Val Leu Phe Glu Thr  
85 90 95  
tac cat cca cgt gga gtt ccg acg tct ctc att caa aag ctg cag att 336  
Tyr His Pro Arg Gly Val Pro Thr Ser Leu Ile Gln Lys Leu Gln Ile  
100 105 110  
gga gtg atg gag gag gag gcg ttt cgg gat tcg ttt tac agt tgg act 384  
Gly Val Met Glu Glu Glu Ala Phe Arg Asp Ser Phe Tyr Ser Trp Thr  
115 120 125  
gat tct gac ttt tat act gtg ttg aag agg agg gtt gtg gag cgg ttg 432  
Asp Ser Asp Phe Tyr Thr Val Leu Lys Arg Arg Val Val Glu Arg Leu  
130 135 140  
gag gag agg ggg ttg gac agg agg gga tcg aaa gag att tgg atc aag 480  
Glu Glu Arg Gly Leu Asp Arg Arg Gly Ser Lys Glu Ile Trp Ile Lys  
145 150 155 160  
gct ttg ttc ttg ttg gtt gga ttt tgg tac tgt ttg tac aag atg tat 528  
Ala Leu Phe Leu Leu Val Gly Phe Trp Tyr Cys Leu Tyr Lys Met Tyr

164

165	170	175	
act acg tcg gat atc gat cag tac ggt att gcc att gcc tat tct att Thr Thr Ser Asp Ile Asp Gln Tyr Gly Ile Ala Ile Ala Tyr Ser Ile 180 185 190			576
gga atg gga acc ttt gcg gca ttc atc ggc acg tgt att caa cac gat Gly Met Gly Thr Phe Ala Ala Phe Ile Gly Thr Cys Ile Gln His Asp 195 200 205			624
gga aat cac ggt gca ttc gct cag aac aag tta ctc aac aag ttg gct Gly Asn His Gly Ala Phe Ala Gln Asn Lys Leu Leu Asn Lys Leu Ala 210 215 220			672
ggg tgg acg ttg gat atg att ggt gcg agt gcg ttt acg tgg gag ctt Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Phe Thr Trp Glu Leu 225 230 235 240			720
cag cac atg ctg ggg cat cat cca tat acg aat gtg ttg gat ggg gtg Gln His Met Leu Gly His His Pro Tyr Thr Asn Val Leu Asp Gly Val 245 250 255			768
gag gag gag agg aag gag agg ggg gag gat gtt gct ttg gaa gaa aag Glu Glu Glu Arg Lys Glu Arg Gly Glu Asp Val Ala Leu Glu Glu Lys 260 265 270			816
gat cag gat ttt gaa gtt gcc aca tcc gga cga tta tat cat att gat Asp Gln Asp Phe Glu Val Ala Thr Ser Gly Arg Leu Tyr His Ile Asp 275 280 285			864
gcc aat gta cgt tat ggt tcg gta tgg aat gtc atg agg ttt tgg gct Ala Asn Val Arg Tyr Gly Ser Val Trp Asn Val Met Arg Phe Trp Ala 290 295 300			912
atg aag gtc att acg atg gga tat atg atg gga tta cca atc tac ttt Met Lys Val Ile Thr Met Gly Tyr Met Met Gly Leu Pro Ile Tyr Phe 305 310 315 320			960
cat gga gta ctg agg gga gtt gga ttg ttt gtt att ggg cat ttg gcg His Gly Val Leu Arg Gly Val Gly Leu Phe Val Ile Gly His Leu Ala 325 330 335			1008
tgt gga gag ttg ttg gcg acg atg ttt att gtg aat cac gtc att gag Cys Gly Glu Leu Leu Ala Thr Met Phe Ile Val Asn His Val Ile Glu 340 345 350			1056
ggt gtg agt tat gga acg aag gat ttg gtt ggt ggt gcg agt cat gta Gly Val Ser Tyr Gly Thr Lys Asp Leu Val Gly Gly Ala Ser His Val 355 360 365			1104
gat gag aag aag att gtc aag cca acg act gta ttg gga gat aca cca Asp Glu Lys Lys Ile Val Lys Pro Thr Thr Val Leu Gly Asp Thr Pro 370 375 380			1152
atg gta aag act cgc gag gag gca ttg aaa agc aac agc aat aac aac Met Val Lys Thr Arg Glu Glu Ala Leu Lys Ser Asn Ser Asn Asn Asn 385 390 395 400			1200
aag aag aag gga gag aag aac tcg gta cca tcc gtt cca ttc aac gac Lys Lys Lys Gly Glu Lys Asn Ser Val Pro Ser Val Pro Phe Asn Asp 405 410 415			1248
tgg gca gca gtc caa tgc cag acc tcc gtg aat tgg tct cca ggc tca Trp Ala Ala Val Gln Cys Gln Thr Ser Val Asn Trp Ser Pro Gly Ser 420 425 430			1296
tgg ttc tgg aat cac ttt tct ggg gga ctc tct cat cag att gag cat Trp Phe Trp Asn His Phe Ser Gly Gly Leu Ser His Gln Ile Glu His			1344

## 165

435                      440                      445  
 cac ttg ttc ccc agc att tgt cat aca aac tac tgt cat atc cag gat      1392  
 His Leu Phe Pro Ser Ile Cys His Thr Asn Tyr Cys His Ile Gln Asp  
 450                      455                      460  
 gtt gtg gag agt acg tgt gct gag tac gga gtt ccg tat cag agt gag      1440  
 Val Val Glu Ser Thr Cys Ala Glu Tyr Gly Val Pro Tyr Gln Ser Glu  
 465                      470                      475                      480  
 agt aat ttg ttt gtt gct tat gga aag atg att agt cat ttg aag ttt      1488  
 Ser Asn Leu Phe Val Ala Tyr Gly Lys Met Ile Ser His Leu Lys Phe  
 485                      490                      495  
 ttg ggt aaa gcc aag tgt gag tag      1512  
 Leu Gly Lys Ala Lys Cys Glu  
 500

<210> 104  
 <211> 503  
 <212> PRT  
 <213> *Thalassiosira pseudonana*

<400> 104

Met Cys Asn Gly Asn Leu Pro Ala Ser Thr Ala Gln Leu Lys Ser Thr  
1                      5                      10                      15

Ser Lys Pro Gln Gln Gln His Glu His Arg Thr Ile Ser Lys Ser Glu  
20                      25                      30

Leu Ala Gln His Asn Thr Pro Lys Ser Ala Trp Cys Ala Val His Ser  
35                      40                      45

Thr Pro Ala Thr Asp Pro Ser His Ser Asn Asn Lys Gln His Ala His  
50                      55                      60

Leu Val Leu Asp Ile Thr Asp Phe Ala Ser Arg His Pro Gly Gly Asp  
65                      70                      75                      80

Leu Ile Leu Leu Ala Ser Gly Lys Asp Ala Ser Val Leu Phe Glu Thr  
85                      90                      95

Tyr His Pro Arg Gly Val Pro Thr Ser Leu Ile Gln Lys Leu Gln Ile  
100                      105                      110

Gly Val Met Glu Glu Glu Ala Phe Arg Asp Ser Phe Tyr Ser Trp Thr  
115                      120                      125

Asp Ser Asp Phe Tyr Thr Val Leu Lys Arg Arg Val Val Glu Arg Leu  
130                      135                      140

Glu Glu Arg Gly Leu Asp Arg Arg Gly Ser Lys Glu Ile Trp Ile Lys  
145                      150                      155                      160

Ala Leu Phe Leu Leu Val Gly Phe Trp Tyr Cys Leu Tyr Lys Met Tyr  
165                      170                      175

Thr Thr Ser Asp Ile Asp Gln Tyr Gly Ile Ala Ile Ala Tyr Ser Ile  
 180 185 190

Gly Met Gly Thr Phe Ala Ala Phe Ile Gly Thr Cys Ile Gln His Asp  
 195 200 205

Gly Asn His Gly Ala Phe Ala Gln Asn Lys Leu Leu Asn Lys Leu Ala  
 210 215 220

Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Phe Thr Trp Glu Leu  
 225 230 235 240

Gln His Met Leu Gly His His Pro Tyr Thr Asn Val Leu Asp Gly Val  
 245 250 255

Glu Glu Glu Arg Lys Glu Arg Gly Glu Asp Val Ala Leu Glu Glu Lys  
 260 265 270

Asp Gln Asp Phe Glu Val Ala Thr Ser Gly Arg Leu Tyr His Ile Asp  
 275 280 285

Ala Asn Val Arg Tyr Gly Ser Val Trp Asn Val Met Arg Phe Trp Ala  
 290 295 300

Met Lys Val Ile Thr Met Gly Tyr Met Met Gly Leu Pro Ile Tyr Phe  
 305 310 315 320

His Gly Val Leu Arg Gly Val Gly Leu Phe Val Ile Gly His Leu Ala  
 325 330 335

Cys Gly Glu Leu Leu Ala Thr Met Phe Ile Val Asn His Val Ile Glu  
 340 345 350

Gly Val Ser Tyr Gly Thr Lys Asp Leu Val Gly Gly Ala Ser His Val  
 355 360 365

Asp Glu Lys Lys Ile Val Lys Pro Thr Thr Val Leu Gly Asp Thr Pro  
 370 375 380

Met Val Lys Thr Arg Glu Glu Ala Leu Lys Ser Asn Ser Asn Asn Asn  
 385 390 395 400

Lys Lys Lys Gly Glu Lys Asn Ser Val Pro Ser Val Pro Phe Asn Asp  
 405 410 415

Trp Ala Ala Val Gln Cys Gln Thr Ser Val Asn Trp Ser Pro Gly Ser  
 420 425 430

Trp Phe Trp Asn His Phe Ser Gly Gly Leu Ser His Gln Ile Glu His  
 435 440 445

His Leu Phe Pro Ser Ile Cys His Thr Asn Tyr Cys His Ile Gln Asp  
 450 455 460

Val Val Glu Ser Thr Cys Ala Glu Tyr Gly Val Pro Tyr Gln Ser Glu  
 465 470 475 480

Ser Asn Leu Phe Val Ala Tyr Gly Lys Met Ile Ser His Leu Lys Phe  
 485 490 495

Leu Gly Lys Ala Lys Cys Glu  
 500

<210> 105  
 <211> 1257  
 <212> DNA  
 <213> *Thalassiosira pseudonana*

<220>  
 <221> CDS  
 <222> (1)..(1257)  
 <223> Omega-3-Desaturase

<400> 105  
 atg tac aga tta aca tcc acc ttc ctc atc gca ttg gca ttc tcc tcc 48  
 Met Tyr Arg Leu Thr Ser Thr Phe Leu Ile Ala Leu Ala Phe Ser Ser  
 1 5 10 15  
 tcc atc aat gcc ttc tct cca caa cgg cca cca cgt act atc acc aaa 96  
 Ser Ile Asn Ala Phe Ser Pro Gln Arg Pro Pro Arg Thr Ile Thr Lys  
 20 25 30  
 agt aaa gtc caa agc acc gtg cta ccc ata ccg acc aag gat gat ctg 144  
 Ser Lys Val Gln Ser Thr Val Leu Pro Ile Pro Thr Lys Asp Asp Leu  
 35 40 45  
 aac ttt ctc caa cca caa ctc gat gag aat gat ctc tac ctc gac gat 192  
 Asn Phe Leu Gln Pro Gln Leu Asp Glu Asn Asp Leu Tyr Leu Asp Asp  
 50 55 60  
 gtc aac act cca cca aga gca ggt acc atc atg aag atg ttg ccg aag 240  
 Val Asn Thr Pro Pro Arg Ala Gly Thr Ile Met Lys Met Leu Pro Lys  
 65 70 75 80  
 gaa acg ttc aac att gat aca gca act tca ttg ggt tac ttt ggt atg 288  
 Glu Thr Phe Asn Ile Asp Thr Ala Thr Ser Leu Gly Tyr Phe Gly Met  
 85 90 95  
 gat atg gca gcg gtt gta tcg tcc atg acg ttg cta aat gct att gta 336  
 Asp Met Ala Ala Val Val Ser Ser Met Thr Leu Leu Asn Ala Ile Val  
 100 105 110  
 act tcg gat cag tac cat gct ctt cca ctt cct ctc caa gca gca aca 384  
 Thr Ser Asp Gln Tyr His Ala Leu Pro Leu Pro Leu Gln Ala Ala Thr  
 115 120 125  
 gtg att ccc ttt cag cta ttg gct ggg ttc gcc atg tgg tgt atg tgg 432  
 Val Ile Pro Phe Gln Leu Leu Ala Gly Phe Ala Met Trp Cys Met Trp  
 130 135 140  
 tgc att gga cac gat gct gga cat tct act gtt tcg aag aca aag tgg 480  
 Cys Ile Gly His Asp Ala Gly His Ser Thr Val Ser Lys Thr Lys Trp

## 168

145	150	155	160	
atc aac cga gtc gtt ggt gaa gtg gct cat tct gtt gtt tgt ctc acg Ile Asn Arg Val Val Gly Glu Val Ala His Ser Val Val Cys Leu Thr 165 170 175				528
ccg ttc gtg cct tgg cag atg tcg cat agg aaa cac cat ttg aat cac Pro Phe Val Pro Trp Gln Met Ser His Arg Lys His His Leu Asn His 180 185 190				576
aat cat att gaa aag gac tac tct cat aag tgg tac agt cgc gac gag Asn His Ile Glu Lys Asp Tyr Ser His Lys Trp Tyr Ser Arg Asp Glu 195 200 205				624
ttt gat gat atc cca caa ctc tat aag aca ttt ggc tac aac cca aga Phe Asp Asp Ile Pro Gln Leu Tyr Lys Thr Phe Gly Tyr Asn Pro Arg 210 215 220				672
atg atg caa ctt cca ttc ctc tac ttc atg tat ctt gca ttg gga att Met Met Gln Leu Pro Phe Leu Tyr Phe Met Tyr Leu Ala Leu Gly Ile 225 230 235 240				720
cca gat ggt ggg cat gtt gtg ttc tac gga aga atg tgg gaa gga gtg Pro Asp Gly Gly His Val Val Phe Tyr Gly Arg Met Trp Glu Gly Val 245 250 255				768
tca ttg cag aag aag ttt gat gct gct att tct gtg gcc gta tca tgt Ser Leu Gln Lys Lys Phe Asp Ala Ala Ile Ser Val Ala Val Ser Cys 260 265 270				816
gca act gct gga tcg ctt tgg atg aat atg ggt aca gca gac ttc acg Ala Thr Ala Gly Ser Leu Trp Met Asn Met Gly Thr Ala Asp Phe Thr 275 280 285				864
gtg gta tgc atg gtt cct tgg cta gtt cta tcg tgg tgg ctc ttc atg Val Val Cys Met Val Pro Trp Leu Val Leu Ser Trp Trp Leu Phe Met 290 295 300				912
gta aca tac ctt cag cat cat tca gaa gac gga aag cta tac act gat Val Thr Tyr Leu Gln His His Ser Glu Asp Gly Lys Leu Tyr Thr Asp 305 310 315 320				960
gaa acg ttt aca ttt gaa aag gga gcc ttc gag acc gtg gat cgt tcg Glu Thr Phe Thr Phe Glu Lys Gly Ala Phe Glu Thr Val Asp Arg Ser 325 330 335				1008
tac ggc aag ttg atc aac cga atg tcg cat cac atg atg gac ggt cac Tyr Gly Lys Leu Ile Asn Arg Met Ser His His Met Met Asp Gly His 340 345 350				1056
gtg gtg cac cac ttg ttc ttt gaa cgt gta cct cac tac aga tta gag Val Val His His Leu Phe Phe Glu Arg Val Pro His Tyr Arg Leu Glu 355 360 365				1104
gca gct acc gaa gct ctt gtg aaa gga atg gat gaa acg gga cag aaa Ala Ala Thr Glu Ala Leu Val Lys Gly Met Asp Glu Thr Gly Gln Lys 370 375 380				1152
cat ttg tac aaa tac att gat act cct gat ttc aat gcc gag att gtc His Leu Tyr Lys Tyr Ile Asp Thr Pro Asp Phe Asn Ala Glu Ile Val 385 390 395 400				1200
aac gga ttt cgc gac aat tgg ttc ctt gtt gaa gag gag aac atc aaa Asn Gly Phe Arg Asp Asn Trp Phe Leu Val Glu Glu Glu Asn Ile Lys 405 410 415				1248
agg gag tag Arg Glu				1257



<210> 106  
 <211> 418  
 <212> PRT  
 <213> *Thalassiosira pseudonana*  
 <400> 106

Met Tyr Arg Leu Thr Ser Thr Phe Leu Ile Ala Leu Ala Phe Ser Ser  
 1 5 10 15

Ser Ile Asn Ala Phe Ser Pro Gln Arg Pro Pro Arg Thr Ile Thr Lys  
 20 25 30

Ser Lys Val Gln Ser Thr Val Leu Pro Ile Pro Thr Lys Asp Asp Leu  
 35 40 45

Asn Phe Leu Gln Pro Gln Leu Asp Glu Asn Asp Leu Tyr Leu Asp Asp  
 50 55 60

Val Asn Thr Pro Pro Arg Ala Gly Thr Ile Met Lys Met Leu Pro Lys  
 65 70 75 80

Glu Thr Phe Asn Ile Asp Thr Ala Thr Ser Leu Gly Tyr Phe Gly Met  
 85 90 95

Asp Met Ala Ala Val Val Ser Ser Met Thr Leu Leu Asn Ala Ile Val  
 100 105 110

Thr Ser Asp Gln Tyr His Ala Leu Pro Leu Pro Leu Gln Ala Ala Thr  
 115 120 125

Val Ile Pro Phe Gln Leu Leu Ala Gly Phe Ala Met Trp Cys Met Trp  
 130 135 140

Cys Ile Gly His Asp Ala Gly His Ser Thr Val Ser Lys Thr Lys Trp  
 145 150 155 160

Ile Asn Arg Val Val Gly Glu Val Ala His Ser Val Val Cys Leu Thr  
 165 170 175

Pro Phe Val Pro Trp Gln Met Ser His Arg Lys His His Leu Asn His  
 180 185 190

Asn His Ile Glu Lys Asp Tyr Ser His Lys Trp Tyr Ser Arg Asp Glu  
 195 200 205

Phe Asp Asp Ile Pro Gln Leu Tyr Lys Thr Phe Gly Tyr Asn Pro Arg  
 210 215 220

Met Met Gln Leu Pro Phe Leu Tyr Phe Met Tyr Leu Ala Leu Gly Ile  
 225 230 235 240

Pro Asp Gly Gly His Val Val Phe Tyr Gly Arg Met Trp Glu Gly Val  
245 250 255

Ser Leu Gln Lys Lys Phe Asp Ala Ala Ile Ser Val Ala Val Ser Cys  
260 265 270

Ala Thr Ala Gly Ser Leu Trp Met Asn Met Gly Thr Ala Asp Phe Thr  
275 280 285

Val Val Cys Met Val Pro Trp Leu Val Leu Ser Trp Trp Leu Phe Met  
290 295 300

Val Thr Tyr Leu Gln His His Ser Glu Asp Gly Lys Leu Tyr Thr Asp  
305 310 315 320

Glu Thr Phe Thr Phe Glu Lys Gly Ala Phe Glu Thr Val Asp Arg Ser  
325 330 335

Tyr Gly Lys Leu Ile Asn Arg Met Ser His His Met Met Asp Gly His  
340 345 350

Val Val His His Leu Phe Phe Glu Arg Val Pro His Tyr Arg Leu Glu  
355 360 365

Ala Ala Thr Glu Ala Leu Val Lys Gly Met Asp Glu Thr Gly Gln Lys  
370 375 380

His Leu Tyr Lys Tyr Ile Asp Thr Pro Asp Phe Asn Ala Glu Ile Val  
385 390 395 400

Asn Gly Phe Arg Asp Asn Trp Phe Leu Val Glu Glu Glu Asn Ile Lys  
405 410 415

Arg Glu

<210> 107

<211> 1086

<212> DNA

<213> *Ostreococcus tauri*

<220>

<221> CDS

<222> (1)..(1086)

<223> Delta-12-Desaturase

<400> 107

atg cag gag ggg gtg cga aac att ccg aac gag tgc ttt gag acg gga  
Met Gln Glu Gly Val Arg Asn Ile Pro Asn Glu Cys Phe Glu Thr Gly  
1 5 10 15

48

cat ctt gaa aga ccc tgg cgt tcc ggc cgg tgt ggg cgc gat ccc ggt  
His Leu Glu Arg Pro Trp Arg Ser Gly Arg Cys Gly Arg Asp Pro Gly

96

171

20	25	30	
tcg aat tgg ggc gct ggc ttc cgc ttt ttt tcg ctc aag ggg ttt tgg Ser Asn Trp Gly Ala Gly Phe Arg Phe Phe Ser Leu Lys Gly Phe Trp 35 40 45			144
tgg ccg gcg tgg tgg gcg tac gcg ttc gtg acg ggg acg gcg gcc act Trp Pro Ala Trp Trp Ala Tyr Ala Phe Val Thr Gly Thr Ala Ala Thr 50 55 60			192
ggg tgt tgg gtc gcc gcg cac gag tgc ggg cac ggc gcg ttc agc gat Gly Cys Trp Val Ala Ala His Glu Cys Gly His Gly Ala Phe Ser Asp 65 70 75 80			240
aac aag acg ttg caa gat gcg gtt gga tac gtg ttg cac tcg ttg ctc Asn Lys Thr Leu Gln Asp Ala Val Gly Tyr Val Leu His Ser Leu Leu 85 90 95			288
ttg gtg ccg tac ttt tct tgg cag cga tca cac gcg gtg cat cac tcg Leu Val Pro Tyr Phe Ser Trp Gln Arg Ser His Ala Val His His Ser 100 105 110			336
agg acg aat cac gtt ctt gag ggc gag acg cac gtg ccg gcg cgc ttg Arg Thr Asn His Val Leu Glu Gly Glu Thr His Val Pro Ala Arg Leu 115 120 125			384
ggg acg gaa gac gcc aac gtc gtg ttc aag ctt cgc gaa ttg atc ggt Gly Thr Glu Asp Ala Asn Val Val Phe Lys Leu Arg Glu Leu Ile Gly 130 135 140			432
gaa ggg ccg ttc acg ttt ttc aac ctc gtc ggc gtc ttc gcg ctc gga Glu Gly Pro Phe Thr Phe Phe Asn Leu Val Gly Val Phe Ala Leu Gly 145 150 155 160			480
tgg ccg att tac ttg ctc acc ggc gcg agc ggc gga ccg gtg cgc ggt Trp Pro Ile Tyr Leu Leu Thr Gly Ala Ser Gly Gly Pro Val Arg Gly 165 170 175			528
aac acg aac cac ttc tta ccc ttc atg ggc gag aaa ggt aag cac gcg Asn Thr Asn His Phe Leu Pro Phe Met Gly Glu Lys Gly Lys His Ala 180 185 190			576
ctg ttc ccg ggt aag tgg gcg aag aag gtg tgg cag tct gac atc ggc Leu Phe Pro Gly Lys Trp Ala Lys Lys Val Trp Gln Ser Asp Ile Gly 195 200 205			624
gtt gtt gcc gtc ctg ggc gcg ctc gcg gct tgg gcg gcg cac agc ggg Val Val Ala Val Leu Gly Ala Leu Ala Ala Trp Ala Ala His Ser Gly 210 215 220			672
att gcc aca gtg atg gca ctc tac gtc ggc ccg tac atg gtg acc aac Ile Ala Thr Val Met Ala Leu Tyr Val Gly Pro Tyr Met Val Thr Asn 225 230 235 240			720
ttt tgg ctc gtc ttg tac acg tgg tta cag cac acc gac gtt gac gtg Phe Trp Leu Val Leu Tyr Thr Trp Leu Gln His Thr Asp Val Asp Val 245 250 255			768
ccg cac ttc gag ggc gac gat tgg aac ttg gtc aag ggg gca ttc atg Pro His Phe Glu Gly Asp Asp Trp Asn Leu Val Lys Gly Ala Phe Met 260 265 270			816
acg atc gat cgc ccg tac ggc cca gtt ttt gat ttc ttg cac cac cgc Thr Ile Asp Arg Pro Tyr Gly Pro Val Phe Asp Phe Leu His His Arg 275 280 285			864
atc ggc agc acg cac gtc gcg cac cac atc aac aca cca ttc ccg cat Ile Gly Ser Thr His Val Ala His His Ile Asn Thr Pro Phe Pro His			912

290 295 300

tac aag gct caa atg gcg acg gat gcg cta aag gag gcg tat ccc gac 960  
 Tyr Lys Ala Gln Met Ala Thr Asp Ala Leu Lys Glu Ala Tyr Pro Asp  
 305 310 315 320

ctc tac ctt tac gat cca act ccg atc gcg acc gct acg tgg cgc gtg 1008  
 Leu Tyr Leu Tyr Asp Pro Thr Pro Ile Ala Thr Ala Thr Trp Arg Val  
 325 330 335

ggg agc aag tgc atc gcc gtc gtg aag aag gga gac gaa tgg gtg ttc 1056  
 Gly Ser Lys Cys Ile Ala Val Val Lys Lys Gly Asp Glu Trp Val Phe  
 340 345 350

acg gat aag caa ctc ccg gtc gcg gcg tga 1086  
 Thr Asp Lys Gln Leu Pro Val Ala Ala  
 355 360

<210> 108  
 <211> 361  
 <212> PRT  
 <213> *Ostreococcus tauri*

<400> 108

Met Gln Glu Gly Val Arg Asn Ile Pro Asn Glu Cys Phe Glu Thr Gly  
 1 5 10 15

His Leu Glu Arg Pro Trp Arg Ser Gly Arg Cys Gly Arg Asp Pro Gly  
 20 25 30

Ser Asn Trp Gly Ala Gly Phe Arg Phe Phe Ser Leu Lys Gly Phe Trp  
 35 40 45

Trp Pro Ala Trp Trp Ala Tyr Ala Phe Val Thr Gly Thr Ala Ala Thr  
 50 55 60

Gly Cys Trp Val Ala Ala His Glu Cys Gly His Gly Ala Phe Ser Asp  
 65 70 75 80

Asn Lys Thr Leu Gln Asp Ala Val Gly Tyr Val Leu His Ser Leu Leu  
 85 90 95

Leu Val Pro Tyr Phe Ser Trp Gln Arg Ser His Ala Val His His Ser  
 100 105 110

Arg Thr Asn His Val Leu Glu Gly Glu Thr His Val Pro Ala Arg Leu  
 115 120 125

Gly Thr Glu Asp Ala Asn Val Val Phe Lys Leu Arg Glu Leu Ile Gly  
 130 135 140

Glu Gly Pro Phe Thr Phe Phe Asn Leu Val Gly Val Phe Ala Leu Gly  
 145 150 155 160

Trp Pro Ile Tyr Leu Leu Thr Gly Ala Ser Gly Gly Pro Val Arg Gly  
 165 170 175

Asn Thr Asn His Phe Leu Pro Phe Met Gly Glu Lys Gly Lys His Ala  
180 185 190

Leu Phe Pro Gly Lys Trp Ala Lys Lys Val Trp Gln Ser Asp Ile Gly  
195 200 205

Val Val Ala Val Leu Gly Ala Leu Ala Ala Trp Ala Ala His Ser Gly  
210 215 220

Ile Ala Thr Val Met Ala Leu Tyr Val Gly Pro Tyr Met Val Thr Asn  
225 230 235 240

Phe Trp Leu Val Leu Tyr Thr Trp Leu Gln His Thr Asp Val Asp Val  
245 250 255

Pro His Phe Glu Gly Asp Asp Trp Asn Leu Val Lys Gly Ala Phe Met  
260 265 270

Thr Ile Asp Arg Pro Tyr Gly Pro Val Phe Asp Phe Leu His His Arg  
275 280 285

Ile Gly Ser Thr His Val Ala His His Ile Asn Thr Pro Phe Pro His  
290 295 300

Tyr Lys Ala Gln Met Ala Thr Asp Ala Leu Lys Glu Ala Tyr Pro Asp  
305 310 315 320

Leu Tyr Leu Tyr Asp Pro Thr Pro Ile Ala Thr Ala Thr Trp Arg Val  
325 330 335

Gly Ser Lys Cys Ile Ala Val Val Lys Lys Gly Asp Glu Trp Val Phe  
340 345 350

Thr Asp Lys Gln Leu Pro Val Ala Ala  
355 360

<210> 109  
<211> 1305  
<212> DNA  
<213> *Thalassiosira pseudonana*

<220>  
<221> CDS  
<222> (1)..(1305)  
<223> Delta-12-Desaturase

<400> 109  
atg gga aag gga gga aga tca gta acc cgc gct caa aca gca gaa aag 48  
Met Gly Lys Gly Gly Arg Ser Val Thr Arg Ala Gln Thr Ala Glu Lys  
1 5 10 15  
tca gca cac acc atc caa acc ttc acc gac ggc cga tgg gtc tcc ccc 96  
Ser Ala His Thr Ile Gln Thr Phe Thr Asp Gly Arg Trp Val Ser Pro

20	25	30	
tac aac ccc ctc gca aaa gat gca cct gaa ctc ccc tcc aag ggt gaa Tyr Asn Pro Leu Ala Lys Asp Ala Pro Glu Leu Pro Ser Lys Gly Glu 35 40 45			144
atc aag gcg gtc atc ccc aaa gag tgc ttc gaa cga agc tac ctc cac Ile Lys Ala Val Ile Pro Lys Glu Cys Phe Glu Arg Ser Tyr Leu His 50 55 60			192
tcc atg tac ttc gtc ctc cgt gac acc gtc atg gcc gtg gcc tgc gcc Ser Met Tyr Phe Val Leu Arg Asp Thr Val Met Ala Val Ala Cys Ala 65 70 75 80			240
tac atc gcc cac tca acg ctc tcc acc gat att ccc tcc gag tta ctg Tyr Ile Ala His Ser Thr Leu Ser Thr Asp Ile Pro Ser Glu Leu Leu 85 90 95			288
agc gtg gac gca ctc aaa tgg ttc ctc gga tgg aac acc tac gcc ttt Ser Val Asp Ala Leu Lys Trp Phe Leu Gly Trp Asn Thr Tyr Ala Phe 100 105 110			336
tgg atg ggg tgc att ctc acc gga cac tgg gtc cta gcc cat gaa tgt Trp Met Gly Cys Ile Leu Thr Gly His Trp Val Leu Ala His Glu Cys 115 120 125			384
gga cat ggt gca ttc tct ccc tct cag acg ttt aat gac ttt tgg ggg Gly His Gly Ala Phe Ser Pro Ser Gln Thr Phe Asn Asp Phe Trp Gly 130 135 140			432
ttc att atg cat cag gcg gtg ttg gtt ccg tat ttc gcc tgg cag tac Phe Ile Met His Gln Ala Val Leu Val Pro Tyr Phe Ala Trp Gln Tyr 145 150 155 160			480
tct cat gcg aag cat cat cga cgt acc aac aac att atg gat ggg gag Ser His Ala Lys His His Arg Arg Thr Asn Asn Ile Met Asp Gly Glu 165 170 175			528
agc cat gtg ccc aat atc gcc aag gaa atg gga ttg aac gag aag aat Ser His Val Pro Asn Ile Ala Lys Glu Met Gly Leu Asn Glu Lys Asn 180 185 190			576
gag cgc agt gga gga tat gcc gcc att cat gag gct att gga gat gga Glu Arg Ser Gly Gly Tyr Ala Ala Ile His Glu Ala Ile Gly Asp Gly 195 200 205			624
ccc ttt gcg atg ttt caa atc ttt gct cac ttg gtg atc ggg tgg cct Pro Phe Ala Met Phe Gln Ile Phe Ala His Leu Val Ile Gly Trp Pro 210 215 220			672
att tac ttg atg gga ttt gct tcc act gga cgt ctc ggt cag gat ggg Ile Tyr Leu Met Gly Phe Ala Ser Thr Gly Arg Leu Gly Gln Asp Gly 225 230 235 240			720
aag gaa ctt cag gct gga gag atc atc gac cat tac cgt cct tgg agt Lys Glu Leu Gln Ala Gly Glu Ile Ile Asp His Tyr Arg Pro Trp Ser 245 250 255			768
aag atg ttc ccc acc aag ttg cga ttc aaa att gct ctt tcg aca ctt Lys Met Phe Pro Thr Lys Leu Arg Phe Lys Ile Ala Leu Ser Thr Leu 260 265 270			816
gga gtg att gcc gcc tgg gtt ggg ttg tac ttt gct gca caa gag tat Gly Val Ile Ala Ala Trp Val Gly Leu Tyr Phe Ala Ala Gln Glu Tyr 275 280 285			864
gga gtc ttg ccc gtg gtt ctt tgg tac att ggc cca ctc atg tgg aat Gly Val Leu Pro Val Val Leu Trp Tyr Ile Gly Pro Leu Met Trp Asn			912

## 175

290	295	300	
cag gcg tgg ctt gtg ctc tac act tgg ctt cag cac aat gat ccc tcc			960
Gln Ala Trp Leu Val	Leu Tyr Thr Trp	Leu Gln His Asn Asp Pro Ser	
305	310	315	320
gtg cct caa tat gga agt gac gaa tgg aca tgg gtc aag gga gct ttg			1008
Val Pro Gln Tyr	Gly Ser Asp Glu Trp Thr Trp	Val Lys Gly Ala Leu	
	325	330	335
tcg acg att gat cgc ccg tat ggt atc ttt gac ttc ttc cat cac aag			1056
Ser Thr Ile Asp Arg Pro Tyr Gly Ile Phe Asp Phe Phe His His Lys			
	340	345	350
att gga agc act cac gta gct cat cat ttg ttc cac gag atg cca ttt			1104
Ile Gly Ser Thr His Val Ala His His Leu Phe His Glu Met Pro Phe			
	355	360	365
tac aag gcg gat gtg gct act gcg tcg atc aag ggt ttc ttg gag ccg			1152
Tyr Lys Ala Asp Val Ala Thr Ala Ser Ile Lys Gly Phe Leu Glu Pro			
	370	375	380
aag gga ctt tac aac tat gat cca acg cct tgg tat gtg gcc atg tgg			1200
Lys Gly Leu Tyr Asn Tyr Asp Pro Thr Pro Trp Tyr Val Ala Met Trp			
	385	390	400
agg gtg gcc aag act tgt cat tat att gag gat gtg gat gga gtt cag			1248
Arg Val Ala Lys Thr Cys His Tyr Ile Glu Asp Val Asp Gly Val Gln			
	405	410	415
tat tat aag agt ttg gag gat gtg cct ttg aag aag gat gcc aag aag			1296
Tyr Tyr Lys Ser Leu Glu Asp Val Pro Leu Lys Lys Asp Ala Lys Lys			
	420	425	430
tct gat tag			1305
Ser Asp			

<210> 110  
 <211> 434  
 <212> PRT  
 <213> *Thalassiosira pseudonana*

<400> 110

Met Gly Lys Gly Gly Arg Ser Val Thr Arg Ala Gln Thr Ala Glu Lys
1 5 10 15

Ser Ala His Thr Ile Gln Thr Phe Thr Asp Gly Arg Trp Val Ser Pro
20 25 30

Tyr Asn Pro Leu Ala Lys Asp Ala Pro Glu Leu Pro Ser Lys Gly Glu
35 40 45

Ile Lys Ala Val Ile Pro Lys Glu Cys Phe Glu Arg Ser Tyr Leu His
50 55 60

Ser Met Tyr Phe Val Leu Arg Asp Thr Val Met Ala Val Ala Cys Ala
65 70 75 80

Tyr Ile Ala His Ser Thr Leu Ser Thr Asp Ile Pro Ser Glu Leu Leu
85 90 95

Ser Val Asp Ala Leu Lys Trp Phe Leu Gly Trp Asn Thr Tyr Ala Phe  
 100 105 110

Trp Met Gly Cys Ile Leu Thr Gly His Trp Val Leu Ala His Glu Cys  
 115 120 125

Gly His Gly Ala Phe Ser Pro Ser Gln Thr Phe Asn Asp Phe Trp Gly  
 130 135 140

Phe Ile Met His Gln Ala Val Leu Val Pro Tyr Phe Ala Trp Gln Tyr  
 145 150 155 160

Ser His Ala Lys His His Arg Arg Thr Asn Asn Ile Met Asp Gly Glu  
 165 170 175

Ser His Val Pro Asn Ile Ala Lys Glu Met Gly Leu Asn Glu Lys Asn  
 180 185 190

Glu Arg Ser Gly Gly Tyr Ala Ala Ile His Glu Ala Ile Gly Asp Gly  
 195 200 205

Pro Phe Ala Met Phe Gln Ile Phe Ala His Leu Val Ile Gly Trp Pro  
 210 215 220

Ile Tyr Leu Met Gly Phe Ala Ser Thr Gly Arg Leu Gly Gln Asp Gly  
 225 230 235 240

Lys Glu Leu Gln Ala Gly Glu Ile Ile Asp His Tyr Arg Pro Trp Ser  
 245 250 255

Lys Met Phe Pro Thr Lys Leu Arg Phe Lys Ile Ala Leu Ser Thr Leu  
 260 265 270

Gly Val Ile Ala Ala Trp Val Gly Leu Tyr Phe Ala Ala Gln Glu Tyr  
 275 280 285

Gly Val Leu Pro Val Val Leu Trp Tyr Ile Gly Pro Leu Met Trp Asn  
 290 295 300

Gln Ala Trp Leu Val Leu Tyr Thr Trp Leu Gln His Asn Asp Pro Ser  
 305 310 315 320

Val Pro Gln Tyr Gly Ser Asp Glu Trp Thr Trp Val Lys Gly Ala Leu  
 325 330 335

Ser Thr Ile Asp Arg Pro Tyr Gly Ile Phe Asp Phe Phe His His Lys  
 340 345 350

Ile Gly Ser Thr His Val Ala His His Leu Phe His Glu Met Pro Phe  
 355 360 365



Tyr Lys Ala Asp Val Ala Thr Ala Ser Ile Lys Gly Phe Leu Glu Pro  
370 375 380

Lys Gly Leu Tyr Asn Tyr Asp Pro Thr Pro Trp Tyr Val Ala Met Trp  
385 390 395 400

Arg Val Ala Lys Thr Cys His Tyr Ile Glu Asp Val Asp Gly Val Gln  
405 410 415

Tyr Tyr Lys Ser Leu Glu Asp Val Pro Leu Lys Lys Asp Ala Lys Lys  
420 425 430

Ser Asp

<210> 111  
<211> 879  
<212> DNA  
<213> *Ostreococcus tauri*

<220>  
<221> CDS  
<222> (1)..(879)  
<223> Delta-6-Elongase

<400> 111  
atg agt ggc tta cgt gca ccc aac ttt tta cac aga ttc tgg aca aag 48  
Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys  
1 5 10 15  
tgg gac tac gcg att tcc aaa gtc gtc ttc acg tgt gcc gac agt ttt 96  
Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe  
20 25 30  
cag tgg gac atc ggg cca gtg agt tcg agt acg gcg cat tta ccc gcc 144  
Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala  
35 40 45  
att gaa tcc cct acc cca ctg gtg act agc ctc ttg ttc tac tta gtc 192  
Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val  
50 55 60  
aca gtt ttc ttg tgg tat ggt cgt tta acc agg agt tca gac aag aaa 240  
Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys  
65 70 75 80  
att aga gag cct acg tgg tta aga aga ttc ata ata tgt cat aat gcg 288  
Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala  
85 90 95  
ttc ttg ata gtc ctc agt ctt tac atg tgc ctt ggt tgt gtg gcc caa 336  
Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln  
100 105 110  
gcg tat cag aat gga tat act tta tgg ggt aat gaa ttc aag gcc acg 384  
Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr  
115 120 125  
gaa act cag ctt gct ctc tac att tac att ttt tac gta agt aaa ata 432  
Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile

130	135	140	
tac gag ttt gta gat	act tac att atg ctt ctc aag aat aac ttg cgg		480
Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg			
145	150	155	160
caa gta agt ttc cta cac att tat cac cac agc acg att tcc ttt att			528
Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile			
	165	170	175
tgg tgg atc att gct cgg agg gct cgg ggt ggt gat gct tac ttc agc			576
Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser			
	180	185	190
gcg gcc ttg aac tca tgg gta cac gtg tgc atg tac acc tat tat cta			624
Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu			
	195	200	205
tta tca acc ctt att gga aaa gaa gat cct aag cgt tcc aac tac ctt			672
Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu			
	210	215	220
tgg tgg ggt cgc cac cta acg caa atg cag atg ctt cag ttt ttc ttc			720
Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe			
	225	230	235
240			
aac gta ctt caa gcg ttg tac tgc gct tgc ttc tct acg tat ccc aag			768
Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys			
	245	250	255
ttt ttg tcc aaa att ctg ctc gtc tat atg atg agc ctt ctc ggc ttg			816
Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu			
	260	265	270
ttt ggg cat ttc tac tat tcc aag cac ata gca gca gct aag ctc cag			864
Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Lys Leu Gln			
	275	280	285
aaa aaa cag cag tga			879
Lys Lys Gln Gln			
	290		

<210> 112  
 <211> 292  
 <212> PRT  
 <213> *Ostreococcus tauri*

<400> 112

Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys  
 1 5 10 15

Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe  
 20 25 30

Gln Trp Asp Ile Gly Pro Val Ser Ser Thr Ala His Leu Pro Ala  
 35 40 45

Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val  
 50 55 60

Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys  
 65 70 75 80

Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala  
85 90 95

Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln  
100 105 110

Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr  
115 120 125

Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile  
130 135 140

Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg  
145 150 155 160

Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile  
165 170 175

Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser  
180 185 190

Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu  
195 200 205

Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu  
210 215 220

Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe  
225 230 235 240

Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys  
245 250 255

Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu  
260 265 270

Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln  
275 280 285

Lys Lys Gln Gln  
290

<210> 113  
<211> 903  
<212> DNA  
<213> *Ostreococcus tauri*

<220>  
<221> CDS  
<222> (1)..(903)  
<223> Delta-5-Elongase

<400> 113  
 atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg ttc gcc gcg tac 48  
 Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr  
 1 5 10 15

gcg tac gcg acg tac gcc tac gcc ttt gag tgg tgg cac gcg aat ggc 96  
 Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly  
 20 25 30

atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tgg ttg agg 144  
 Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg  
 35 40 45

ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga 192  
 Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly  
 50 55 60

ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg 240  
 Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met  
 65 70 75 80

ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg 288  
 Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly  
 85 90 95

atg ttc gcg cga gag atc tgg ggg ctg ggg cag ccc gtg tgg ggg tca 336  
 Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser  
 100 105 110

acc atg ccg tgg agc gat aga aaa tgg ttt aag atc ctc ctc ggg gtg 384  
 Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val  
 115 120 125

tgg ttg cac tac aac aac aaa tat ttg gag cta ttg gac act gtg ttc 432  
 Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe  
 130 135 140

atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat 480  
 Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr  
 145 150 155 160

cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg 528  
 His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met  
 165 170 175

gcc acg aac gat tgt atc gat gcc tac ttc gcc gcg gcg tgc aac tgc 576  
 Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser  
 180 185 190

ttc att cac atc gtg atg tac tgg tat tat ctc atg tgg gcg ctc ggc 624  
 Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly  
 195 200 205

att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa 672  
 Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln  
 210 215 220

ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac 720  
 Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His  
 225 230 235 240

tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg 768  
 Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met  
 245 250 255

ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tgg aac aag tgc 816  
 Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser

181

260 265 270  
 cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg 864  
 Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala  
 275 280 285  
 ccc agc gtg cga cgc acg cga tct cga aaa att gac taa 903  
 Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp  
 290 295 300  
  
 <210> 114  
 <211> 300  
 <212> PRT  
 <213> *Ostreococcus tauri*  
  
 <400> 114  
 Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr  
 1 5 10 15  
 Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly  
 20 25 30  
 Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg  
 35 40 45  
 Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly  
 50 55 60  
 Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met  
 65 70 75 80  
 Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly  
 85 90 95  
 Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser  
 100 105 110  
 Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val  
 115 120 125  
 Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe  
 130 135 140  
 Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr  
 145 150 155 160  
 His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met  
 165 170 175  
 Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser  
 180 185 190  
 Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly  
 195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln  
210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His  
225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met  
245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser  
260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala  
275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp  
290 295 300

<210> 115

<211> 13

<212> PRT

<213> Konsensus

<220>

<221> MISC\_FEATURE

<222> (1)..(13)

<223> Xaa in der Sequenz an der Position 2, 3, 4, 6, 7, 8 und 9 hat die  
in Tabelle A wiedergegebene Bedeutung.

<400> 115

Asn Xaa Xaa Xaa His Xaa Xaa Met Tyr Xaa Tyr Tyr Xaa  
1 5 10

<210> 116

<211> 10

<212> PRT

<213> Konsensus

<220>

<221> MISC\_FEATURE

<222> (1)..(10)

<223> Xaa an der Position 3, 4, 5 und 6 in der Sequenz hat die in Tabel  
le A wiedergegebene Bedeutung.

<400> 116

His His Xaa Xaa Xaa Xaa Trp Ala Trp Trp  
1 5 10

<210> 117

<211> 909

<212> DNA

<213> Xenopus laevis

<220>

<221> CDS  
 <222> (1)..(909)  
 <223> Delta-5-Elongase

<400> 117  
 atg gcc ttc aag gag ctc aca tca agg gca gtg ctc ctg tat gat gaa 48  
 Met Ala Phe Lys Glu Leu Thr Ser Arg Ala Val Leu Leu Tyr Asp Glu  
 1 5 10 15

tgg att aaa gat gct gat cct agg gtt gaa gac tgg cca ctc atg tcc 96  
 Trp Ile Lys Asp Ala Asp Pro Arg Val Glu Asp Trp Pro Leu Met Ser  
 20 25 30

tct cct atc cta caa acc atc atc atc ggc gct tac atc tac ttt gtc 144  
 Ser Pro Ile Leu Gln Thr Ile Ile Ile Gly Ala Tyr Ile Tyr Phe Val  
 35 40 45

aca tca ttg ggc cca agg atc atg gag aac agg aag ccg ttt gct ctg 192  
 Thr Ser Leu Gly Pro Arg Ile Met Glu Asn Arg Lys Pro Phe Ala Leu  
 50 55 60

aag gag atc atg gca tgt tac aac tta ttc atg gtt ctg ttt tct gtg 240  
 Lys Glu Ile Met Ala Cys Tyr Asn Leu Phe Met Val Leu Phe Ser Val  
 65 70 75 80

tac atg tgc tat gag ttt ctc atg tgc ggc tgg gct act gga tat tcc 288  
 Tyr Met Cys Tyr Glu Phe Leu Met Ser Gly Trp Ala Thr Gly Tyr Ser  
 85 90 95

ttt aga tgt gac att gtt gac tac tct cag tca cct cag gcg tta cgg 336  
 Phe Arg Cys Asp Ile Val Asp Tyr Ser Gln Ser Pro Gln Ala Leu Arg  
 100 105 110

atg gcc tgg acc tgc tgg ctc ttc tat ttt tca aag ttc att gaa tta 384  
 Met Ala Trp Thr Cys Trp Leu Phe Tyr Phe Ser Lys Phe Ile Glu Leu  
 115 120 125

tta gac act gtt ttc ttt gtg ctg cgt aag aag aac agc cag att aca 432  
 Leu Asp Thr Val Phe Phe Val Leu Arg Lys Lys Asn Ser Gln Ile Thr  
 130 135 140

ttc ctg cac gtc tat cac cac tcc att atg cct tgg acg tgg tgg ttt 480  
 Phe Leu His Val Tyr His His Ser Ile Met Pro Trp Thr Trp Trp Phe  
 145 150 155 160

gga gtc aaa ttt gct cca ggt ggt ttg ggc aca ttc cat gca ctg gtg 528  
 Gly Val Lys Phe Ala Pro Gly Gly Leu Gly Thr Phe His Ala Leu Val  
 165 170 175

aac tgt gtg gtc cat gtt atc atg tac agc tac tac ggc ctg tca gcc 576  
 Asn Cys Val Val His Val Ile Met Tyr Ser Tyr Tyr Gly Leu Ser Ala  
 180 185 190

ttg ggg cct gcc tac cag aag tac ctg tgg tgg aaa aag tac atg acg 624  
 Leu Gly Pro Ala Tyr Gln Lys Tyr Leu Trp Trp Lys Lys Tyr Met Thr  
 195 200 205

tct atc caa ctg acc cag ttc ttg atg gtt act ttt cac atc ggc cag 672  
 Ser Ile Gln Leu Thr Gln Phe Leu Met Val Thr Phe His Ile Gly Gln  
 210 215 220

ttc ttc ttc atg gag aat tgc ccg tac cag tat ccc gtc ttc ttg tat 720  
 Phe Phe Phe Met Glu Asn Cys Pro Tyr Gln Tyr Pro Val Phe Leu Tyr  
 225 230 235 240

gtc att tgg ctg tac ggg ttc gtt ttc tta atc ttg ttc ctc aac ttc 768  
 Val Ile Trp Leu Tyr Gly Phe Val Phe Leu Ile Leu Phe Leu Asn Phe

184

245	250	255	
tgg ttc cac gct tac atc aaa gga cag agg ctg ccg aaa gcc gtc caa			816
Trp Phe His Ala Tyr Ile Lys Gly Gln Arg Leu Pro Lys Ala Val Gln			
260	265	270	
aat ggc cac tgc aag aac aac aac aac caa gaa aac act tgg tgc aag			864
Asn Gly His Cys Lys Asn Asn Asn Asn Gln Glu Asn Thr Trp Cys Lys			
275	280	285	
aac aaa aac cag aaa aac ggt gca ttg aaa agc aaa aac cat tga			909
Asn Lys Asn Gln Lys Asn Gly Ala Leu Lys Ser Lys Asn His			
290	295	300	
<210>	118		
<211>	302		
<212>	PRT		
<213>	Xenopus laevis		
<400>	118		
Met Ala Phe Lys Glu Leu Thr Ser Arg Ala Val Leu Leu Tyr Asp Glu			
1	5	10	15
Trp Ile Lys Asp Ala Asp Pro Arg Val Glu Asp Trp Pro Leu Met Ser			
20	25	30	
Ser Pro Ile Leu Gln Thr Ile Ile Ile Gly Ala Tyr Ile Tyr Phe Val			
35	40	45	
Thr Ser Leu Gly Pro Arg Ile Met Glu Asn Arg Lys Pro Phe Ala Leu			
50	55	60	
Lys Glu Ile Met Ala Cys Tyr Asn Leu Phe Met Val Leu Phe Ser Val			
65	70	75	80
Tyr Met Cys Tyr Glu Phe Leu Met Ser Gly Trp Ala Thr Gly Tyr Ser			
85	90	95	
Phe Arg Cys Asp Ile Val Asp Tyr Ser Gln Ser Pro Gln Ala Leu Arg			
100	105	110	
Met Ala Trp Thr Cys Trp Leu Phe Tyr Phe Ser Lys Phe Ile Glu Leu			
115	120	125	
Leu Asp Thr Val Phe Phe Val Leu Arg Lys Lys Asn Ser Gln Ile Thr			
130	135	140	
Phe Leu His Val Tyr His His Ser Ile Met Pro Trp Thr Trp Trp Phe			
145	150	155	160
Gly Val Lys Phe Ala Pro Gly Gly Leu Gly Thr Phe His Ala Leu Val			
165	170	175	
Asn Cys Val Val His Val Ile Met Tyr Ser Tyr Tyr Gly Leu Ser Ala			
180	185	190	



Leu Gly Pro Ala Tyr Gln Lys Tyr Leu Trp Trp Lys Lys Tyr Met Thr  
 195 200 205

Ser Ile Gln Leu Thr Gln Phe Leu Met Val Thr Phe His Ile Gly Gln  
 210 215 220

Phe Phe Phe Met Glu Asn Cys Pro Tyr Gln Tyr Pro Val Phe Leu Tyr  
 225 230 235 240

Val Ile Trp Leu Tyr Gly Phe Val Phe Leu Ile Leu Phe Leu Asn Phe  
 245 250 255

Trp Phe His Ala Tyr Ile Lys Gly Gln Arg Leu Pro Lys Ala Val Gln  
 260 265 270

Asn Gly His Cys Lys Asn Asn Asn Asn Gln Glu Asn Thr Trp Cys Lys  
 275 280 285

Asn Lys Asn Gln Lys Asn Gly Ala Leu Lys Ser Lys Asn His  
 290 295 300

<210> 119  
 <211> 870  
 <212> DNA  
 <213> *Ciona intestinalis*

<220>  
 <221> CDS  
 <222> (1)..(870)  
 <223> Delta-5-Elongase

<400> 119  
 atg gac gta ctt cat cgt ttc tta gga ttc tac gaa tgg acg ctg act 48  
 Met Asp Val Leu His Arg Phe Leu Gly Phe Tyr Glu Trp Thr Leu Thr  
 1 5 10 15  
 ttc gcg gac ccc cga gtg gca aaa tgg cct tta ata gaa aac ccc ctt 96  
 Phe Ala Asp Pro Arg Val Ala Lys Trp Pro Leu Ile Glu Asn Pro Leu  
 20 25 30  
 cct aca att gct att gtg ttg ctg tac ctg gcg ttt gtt ctg tat att 144  
 Pro Thr Ile Ala Ile Val Leu Leu Tyr Leu Ala Phe Val Leu Tyr Ile  
 35 40 45  
 ggg ccg cgt ttt atg cga aaa aga gca cca gtt gac ttt ggt tta ttc 192  
 Gly Pro Arg Phe Met Arg Lys Arg Ala Pro Val Asp Phe Gly Leu Phe  
 50 55 60  
 ctc cct gga tat aac ttt gct ttg gtt gca tta aat tat tat atc ctg 240  
 Leu Pro Gly Tyr Asn Phe Ala Leu Val Ala Leu Asn Tyr Tyr Ile Leu  
 65 70 75 80  
 caa gaa gtg gtc act ggg agt tat ggg gct ggg tat gat ttg gtt tgc 288  
 Gln Glu Val Val Thr Gly Ser Tyr Gly Ala Gly Tyr Asp Leu Val Cys  
 85 90 95  
 aca cca ctt cga agt gat tcc tac gat ccc aat gaa atg aag gtt gca 336  
 Thr Pro Leu Arg Ser Asp Ser Tyr Asp Pro Asn Glu Met Lys Val Ala

186

100	105	110	
aac gct gta tgg tgg tat tat gta tcc aag ata ata gag ttg ttt gat			384
Asn Ala Val Trp Trp Tyr Tyr Val Ser Lys Ile Ile Glu Leu Phe Asp			
115	120	125	
act gtg ttg ttc act cta cgc aaa cga gac cga caa gta act ttc ctt			432
Thr Val Leu Phe Thr Leu Arg Lys Arg Asp Arg Gln Val Thr Phe Leu			
130	135	140	
cat gtt tat cac cat tct acc atg ccc ctg ttg tgg tgg att ggg gca			480
His Val Tyr His His Ser Thr Met Pro Leu Leu Trp Trp Ile Gly Ala			
145	150	155	160
aag tgg gtg cct ggt ggg caa tca ttt gtt ggc atc ata ctg aac tcc			528
Lys Trp Val Pro Gly Gly Gln Ser Phe Val Gly Ile Ile Leu Asn Ser			
	165	170	175
agt gtt cat gtt atc atg tat acg tac tat gga ttg tca gcc ttg ggg			576
Ser Val His Val Ile Met Tyr Thr Tyr Tyr Gly Leu Ser Ala Leu Gly			
	180	185	190
cct cac atg cag aag ttt cta tgg tgg aag aaa tat atc aca atg ttg			624
Pro His Met Gln Lys Phe Leu Trp Trp Lys Lys Tyr Ile Thr Met Leu			
	195	200	205
caa ctg gtt caa ttt gtt ctt gcc atc tac cat act gct cga tca ttg			672
Gln Leu Val Gln Phe Val Leu Ala Ile Tyr His Thr Ala Arg Ser Leu			
	210	215	220
tac gtt aaa tgt ccc tcg cct gtt tgg atg cac tgg gca ctt atc ttg			720
Tyr Val Lys Cys Pro Ser Pro Val Trp Met His Trp Ala Leu Ile Leu			
	225	230	235
tac gct ttc tca ttc att ttg ctt ttc tca aac ttc tac atg cat gcc			768
Tyr Ala Phe Ser Phe Ile Leu Leu Phe Ser Asn Phe Tyr Met His Ala			
	245	250	255
tat atc aag aaa tca aga aaa ggg aaa gag aat ggc agt cga gga aaa			816
Tyr Ile Lys Lys Ser Arg Lys Gly Lys Glu Asn Gly Ser Arg Gly Lys			
	260	265	270
ggt ggt gta agt aat gga aag gaa aag ctg cac gct aat ggt aaa acc			864
Gly Gly Val Ser Asn Gly Lys Glu Lys Leu His Ala Asn Gly Lys Thr			
	275	280	285
gat taa			870
Asp			

&lt;210&gt; 120

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Ciona intestinalis

&lt;400&gt; 120

Met Asp Val Leu His Arg Phe Leu Gly Phe Tyr Glu Trp Thr Leu Thr
1 5 10 15

Phe Ala Asp Pro Arg Val Ala Lys Trp Pro Leu Ile Glu Asn Pro Leu
20 25 30

Pro Thr Ile Ala Ile Val Leu Leu Tyr Leu Ala Phe Val Leu Tyr Ile
35 40 45

Gly Pro Arg Phe Met Arg Lys Arg Ala Pro Val Asp Phe Gly Leu Phe  
 50 55 60  
 Leu Pro Gly Tyr Asn Phe Ala Leu Val Ala Leu Asn Tyr Tyr Ile Leu  
 65 70 75 80  
 Gln Glu Val Val Thr Gly Ser Tyr Gly Ala Gly Tyr Asp Leu Val Cys  
 85 90 95  
 Thr Pro Leu Arg Ser Asp Ser Tyr Asp Pro Asn Glu Met Lys Val Ala  
 100 105 110  
 Asn Ala Val Trp Trp Tyr Tyr Val Ser Lys Ile Ile Glu Leu Phe Asp  
 115 120 125  
 Thr Val Leu Phe Thr Leu Arg Lys Arg Asp Arg Gln Val Thr Phe Leu  
 130 135 140  
 His Val Tyr His His Ser Thr Met Pro Leu Leu Trp Trp Ile Gly Ala  
 145 150 155 160  
 Lys Trp Val Pro Gly Gly Gln Ser Phe Val Gly Ile Ile Leu Asn Ser  
 165 170 175  
 Ser Val His Val Ile Met Tyr Thr Tyr Tyr Gly Leu Ser Ala Leu Gly  
 180 185 190  
 Pro His Met Gln Lys Phe Leu Trp Trp Lys Lys Tyr Ile Thr Met Leu  
 195 200 205  
 Gln Leu Val Gln Phe Val Leu Ala Ile Tyr His Thr Ala Arg Ser Leu  
 210 215 220  
 Tyr Val Lys Cys Pro Ser Pro Val Trp Met His Trp Ala Leu Ile Leu  
 225 230 235 240  
 Tyr Ala Phe Ser Phe Ile Leu Leu Phe Ser Asn Phe Tyr Met His Ala  
 245 250 255  
 Tyr Ile Lys Lys Ser Arg Lys Gly Lys Glu Asn Gly Ser Arg Gly Lys  
 260 265 270  
 Gly Gly Val Ser Asn Gly Lys Glu Lys Leu His Ala Asn Gly Lys Thr  
 275 280 285

Asp

&lt;210&gt; 121

&lt;211&gt; 30

<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(30)  
<223>

<400> 121  
aggatccatg gccttcaagg agctcacatc

30

<210> 122  
<211> 35  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(35)  
<223>

<400> 122  
cctcgagtca atgggttttg cttttcaatg caccg

35

<210> 123  
<211> 25  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(25)  
<223>

<400> 123  
taagcttatg gacgtacttc atcgt

25

<210> 124  
<211> 26  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(26)  
<223>

<400> 124  
tcagatcttt aatcggtttt accatt

26

<210> 125  
<211> 34  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(34)  
<223>

<400> 125  
gcggccgcac catggccttc aaggagctca catc 34

<210> 126  
<211> 38  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(38)  
<223>

<400> 126  
gcggccgcct tcaatggttt ttgcttttca atgcaccg 38

<210> 127  
<211> 29  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(29)  
<223>

<400> 127  
gcggccgcac catggacgta cttcatcgt 29

<210> 128  
<211> 27  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(27)  
<223>

<400> 128  
gcggccgctt taatcggttt taccatt 27

<210> 129  
<211> 60  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(60)  
<223>

<400> 129  
gtcgaccgcg ggactagtgg gccctctaga cccgggggat cggatctgc tggctatgaa 60

<210> 130  
<211> 60  
<212> DNA

<213> Primer

<220>

<221> misc\_feature

<222> (1)..(60)

<223>

<400> 130

gtcgaccgcg gcactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa 60

<210> 131

<211> 789

<212> DNA

<213> *Euglena gracilis*

<220>

<221> CDS

<222> (1)..(789)

<223> Delta-5-Elongase

<400> 131

atg ctg ggg gcc atc gcg gac gtc gtg ctc cgg ggg ccc gcc gca ttc 48  
Met Leu Gly Ala Ile Ala Asp Val Val Leu Arg Gly Pro Ala Ala Phe  
1 5 10 15

cac tgg gac cct gcc acc acc ccg ctc gca tcg atc gtc agc ccc tgt 96  
His Trp Asp Pro Ala Thr Thr Pro Leu Ala Ser Ile Val Ser Pro Cys  
20 25 30

gtg gcc tcc gtg gcg tac ctg ggg gcc atc ggg ctg ctg aag cgc cgc 144  
Val Ala Ser Val Ala Tyr Leu Gly Ala Ile Gly Leu Leu Lys Arg Arg  
35 40 45

act gga ccg gag gtc cgc tcc aag ccc ttc gag ctg cta cac aac ggg 192  
Thr Gly Pro Glu Val Arg Ser Lys Pro Phe Glu Leu Leu His Asn Gly  
50 55 60

ctg ctg gtg ggc tgg tcc ctc gtg gtg ctg ctc ggg acg ctg tac ggc 240  
Leu Leu Val Gly Trp Ser Leu Val Val Leu Leu Gly Thr Leu Tyr Gly  
65 70 75 80

gcg ttc cag cgc gtg cag gag gac ggc cgg ggg gtg cag gcc ctc ctg 288  
Ala Phe Gln Arg Val Gln Glu Asp Gly Arg Gly Val Gln Ala Leu Leu  
85 90 95

tgc acc cag cgg cca cca tct cag atc tgg gac ggc ccg gtg ggg tac 336  
Cys Thr Gln Arg Pro Pro Ser Gln Ile Trp Asp Gly Pro Val Gly Tyr  
100 105 110

ttc acg tac ctc ttc tac ctc gcg aag tac tgg gag ctg gcg gac act 384  
Phe Thr Tyr Leu Phe Tyr Leu Ala Lys Tyr Trp Glu Leu Ala Asp Thr  
115 120 125

gtc atc ctc gcc ctc cgc cag aag ccc acc atc ccc ctc cac gtc tac 432  
Val Ile Leu Ala Leu Arg Gln Lys Pro Thr Ile Pro Leu His Val Tyr  
130 135 140

cat cac gcc gtc atg ctg ttc atc gtg tgg tcg tgg ttc gcg cac ccc 480  
His His Ala Val Met Leu Phe Ile Val Trp Ser Trp Phe Ala His Pro  
145 150 155 160

tgg ctc gag ggg agc tgg tgg tgc tcc ctg gtc aac tct ttc atc cac 528  
Trp Leu Glu Gly Ser Trp Trp Cys Ser Leu Val Asn Ser Phe Ile His  
165 170 175

## 191

acg gtg atg tac tcg tac tac acc ctg acg gtg gtt ggc atc aac cct 576  
 Thr Val Met Tyr Ser Tyr Tyr Thr Leu Thr Val Val Gly Ile Asn Pro  
 180 185 190

tgg tgg aag aag tgg atg acc acc atg cag atc atc cag ttc atc acg 624  
 Trp Trp Lys Lys Trp Met Thr Thr Met Gln Ile Ile Gln Phe Ile Thr  
 195 200 205

ggc tgc gtg tac gtc atg gcg ttc ttc ggc cta tat tat gcc ggg gcg 672  
 Gly Cys Val Tyr Val Met Ala Phe Phe Gly Leu Tyr Tyr Ala Gly Ala  
 210 215 220

ggc tgc acc tcc aac gtg tac act gcc tgg ttc tcg atg ggg gtc aac 720  
 Gly Cys Thr Ser Asn Val Tyr Thr Ala Trp Phe Ser Met Gly Val Asn  
 225 230 235 240

ctc agc ttt ctg tgg ctc ttc gct ctt ttc ttc cgc cgg tca tac agc 768  
 Leu Ser Phe Leu Trp Leu Phe Ala Leu Phe Phe Arg Arg Ser Tyr Ser  
 245 250 255

aaa cct agc cgg aag gag tag 789  
 Lys Pro Ser Arg Lys Glu  
 260

<210> 132  
 <211> 262  
 <212> PRT  
 <213> Euglena gracilis

<400> 132

Met Leu Gly Ala Ile Ala Asp Val Val Leu Arg Gly Pro Ala Ala Phe  
 1 5 10 15

His Trp Asp Pro Ala Thr Thr Pro Leu Ala Ser Ile Val Ser Pro Cys  
 20 25 30

Val Ala Ser Val Ala Tyr Leu Gly Ala Ile Gly Leu Leu Lys Arg Arg  
 35 40 45

Thr Gly Pro Glu Val Arg Ser Lys Pro Phe Glu Leu Leu His Asn Gly  
 50 55 60

Leu Leu Val Gly Trp Ser Leu Val Val Leu Leu Gly Thr Leu Tyr Gly  
 65 70 75 80

Ala Phe Gln Arg Val Gln Glu Asp Gly Arg Gly Val Gln Ala Leu Leu  
 85 90 95

Cys Thr Gln Arg Pro Pro Ser Gln Ile Trp Asp Gly Pro Val Gly Tyr  
 100 105 110

Phe Thr Tyr Leu Phe Tyr Leu Ala Lys Tyr Trp Glu Leu Ala Asp Thr  
 115 120 125

Val Ile Leu Ala Leu Arg Gln Lys Pro Thr Ile Pro Leu His Val Tyr  
 130 135 140

## 192

His His Ala Val Met Leu Phe Ile Val Trp Ser Trp Phe Ala His Pro  
145 150 155 160

Trp Leu Glu Gly Ser Trp Trp Cys Ser Leu Val Asn Ser Phe Ile His  
165 170 175

Thr Val Met Tyr Ser Tyr Tyr Thr Leu Thr Val Val Gly Ile Asn Pro  
180 185 190

Trp Trp Lys Lys Trp Met Thr Thr Met Gln Ile Ile Gln Phe Ile Thr  
195 200 205

Gly Cys Val Tyr Val Met Ala Phe Phe Gly Leu Tyr Tyr Ala Gly Ala  
210 215 220

Gly Cys Thr Ser Asn Val Tyr Thr Ala Trp Phe Ser Met Gly Val Asn  
225 230 235 240

Leu Ser Phe Leu Trp Leu Phe Ala Leu Phe Phe Arg Arg Ser Tyr Ser  
245 250 255

Lys Pro Ser Arg Lys Glu  
260

<210> 133  
<211> 789  
<212> DNA  
<213> *Euglena gracilis*

<220>  
<221> CDS  
<222> (1)..(789)  
<223> Delta-5-Elongase

<400> 133  
atg ctg ggg gcc atc gcg gac gtc gtg ctc cgg ggg ccc gcc gca ttc 48  
Met Leu Gly Ala Ile Ala Asp Val Val Leu Arg Gly Pro Ala Ala Phe  
1 5 10 15  
cac tgg gac cct gcc acc acc ccg ctc gca tcg atc gtc agc ccc tgt 96  
His Trp Asp Pro Ala Thr Thr Pro Leu Ala Ser Ile Val Ser Pro Cys  
20 25 30  
gtg gcc tcc gtg gcg tac ctg ggg gcc atc ggg ctg ctg aag cgc cgc 144  
Val Ala Ser Val Ala Tyr Leu Gly Ala Ile Gly Leu Leu Lys Arg Arg  
35 40 45  
act gga ccg gag gtc cgc tcc aag ccc ttc gag ctg cta cac aac ggg 192  
Thr Gly Pro Glu Val Arg Ser Lys Pro Phe Glu Leu Leu His Asn Gly  
50 55 60  
ctg ctg gtg ggc tgg tcc ctc gtg gtg ctg ctc ggg acg ctg tac ggc 240  
Leu Leu Val Gly Trp Ser Leu Val Val Leu Leu Gly Thr Leu Tyr Gly  
65 70 75 80  
gcg tac cag cgc gtg cag gag gac ggc cgg ggg gtg cag gcc ctg ctg 288  
Ala Tyr Gln Arg Val Gln Glu Asp Gly Arg Gly Val Gln Ala Leu Leu  
85 90 95



## 193

tgc acc cag cgg cca cca tct cag atc tgg gac ggc ccg gtg ggg tac 336  
 Cys Thr Gln Arg Pro Pro Ser Gln Ile Trp Asp Gly Pro Val Gly Tyr  
                   100                  105                  110

ttc acg tac ctt ttc tac ctc gcg aag tac tgg gag ctg gtg gac act 384  
 Phe Thr Tyr Leu Phe Tyr Leu Ala Lys Tyr Trp Glu Leu Val Asp Thr  
                   115                  120                  125

gtc atc ctc gcc ctc cgc cag aag ccc acc atc ccc ctc cac gtc tac 432  
 Val Ile Leu Ala Leu Arg Gln Lys Pro Thr Ile Pro Leu His Val Tyr  
                   130                  135                  140

cat cac gcc gtc atg ctg ttc att gtg tgg tgc tgg ttc gcg cac ccc 480  
 His His Ala Val Met Leu Phe Ile Val Trp Ser Trp Phe Ala His Pro  
                   145                  150                  155                  160

tgg ctc gag ggg agc tgg tgg tgc tcc ctg gtc aac tct ttc atc cac 528  
 Trp Leu Glu Gly Ser Trp Trp Cys Ser Leu Val Asn Ser Phe Ile His  
                   165                  170                  175

acg gtg atg tac tcg tat tac acc ctg acg gtg gtt ggc atc aac cct 576  
 Thr Val Met Tyr Ser Tyr Tyr Thr Leu Thr Val Val Gly Ile Asn Pro  
                   180                  185                  190

tgg tgg aag aag tgg atg acc acc atg cag atc atc cag ttc atc acg 624  
 Trp Trp Lys Lys Trp Met Thr Thr Met Gln Ile Ile Gln Phe Ile Thr  
                   195                  200                  205

ggc tgc gtg tac gtc acg gcg ttc ttc ggc cta tac tat gcc ggg gcg 672  
 Gly Cys Val Tyr Val Thr Ala Phe Phe Gly Leu Tyr Tyr Ala Gly Ala  
                   210                  215                  220

ggc tgc acc tcc aac gtg tac act gcc tgg ttc tcg atg ggg gtc aac 720  
 Gly Cys Thr Ser Asn Val Tyr Thr Ala Trp Phe Ser Met Gly Val Asn  
                   225                  230                  235                  240

ctc agc ttt ctg tgg ctc ttc gct ctt ttc ttc cgc cgg tcg tac agc 768  
 Leu Ser Phe Leu Trp Leu Phe Ala Leu Phe Phe Arg Arg Ser Tyr Ser  
                   245                  250                  255

aaa cct agc cgg aag gag tag 789  
 Lys Pro Ser Arg Lys Glu  
                   260

<210> 134  
 <211> 262  
 <212> PRT  
 <213> Euglena gracilis

<400> 134

Met Leu Gly Ala Ile Ala Asp Val Val Leu Arg Gly Pro Ala Ala Phe  
 1                  5                  10                  15

His Trp Asp Pro Ala Thr Thr Pro Leu Ala Ser Ile Val Ser Pro Cys  
                   20                  25                  30

Val Ala Ser Val Ala Tyr Leu Gly Ala Ile Gly Leu Leu Lys Arg Arg  
                   35                  40                  45

Thr Gly Pro Glu Val Arg Ser Lys Pro Phe Glu Leu Leu His Asn Gly  
                   50                  55                  60

## 194

Leu Leu Val Gly Trp Ser Leu Val Val Leu Leu Gly Thr Leu Tyr Gly  
65 70 75 80

Ala Tyr Gln Arg Val Gln Glu Asp Gly Arg Gly Val Gln Ala Leu Leu  
85 90 95

Cys Thr Gln Arg Pro Pro Ser Gln Ile Trp Asp Gly Pro Val Gly Tyr  
100 105 110

Phe Thr Tyr Leu Phe Tyr Leu Ala Lys Tyr Trp Glu Leu Val Asp Thr  
115 120 125

Val Ile Leu Ala Leu Arg Gln Lys Pro Thr Ile Pro Leu His Val Tyr  
130 135 140

His His Ala Val Met Leu Phe Ile Val Trp Ser Trp Phe Ala His Pro  
145 150 155 160

Trp Leu Glu Gly Ser Trp Trp Cys Ser Leu Val Asn Ser Phe Ile His  
165 170 175

Thr Val Met Tyr Ser Tyr Tyr Thr Leu Thr Val Val Gly Ile Asn Pro  
180 185 190

Trp Trp Lys Lys Trp Met Thr Thr Met Gln Ile Ile Gln Phe Ile Thr  
195 200 205

Gly Cys Val Tyr Val Thr Ala Phe Phe Gly Leu Tyr Tyr Ala Gly Ala  
210 215 220

Gly Cys Thr Ser Asn Val Tyr Thr Ala Trp Phe Ser Met Gly Val Asn  
225 230 235 240

Leu Ser Phe Leu Trp Leu Phe Ala Leu Phe Phe Arg Arg Ser Tyr Ser  
245 250 255

Lys Pro Ser Arg Lys Glu  
260

<210> 135

<211> 897

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(897)

<223> Delta-5-Elongase

<400> 135

atg gca tct gtt tac tcc acc cta acc tac tgg ctc gtc cac cac ccc  
Met Ala Ser Val Tyr Ser Thr Leu Thr Tyr Trp Leu Val His His Pro  
1 5 10 15

## 195

tac att gcc aac ttc acg tgg acc gaa ggt gaa aca cta ggc tcc acc Tyr Ile Ala Asn Phe Thr Trp Thr Glu Gly Glu Thr Leu Gly Ser Thr 20 25 30	96
gtt ttc ttt gtc ttt gtc gtc gtc tcc ctt tac ctc tcc gcc aca ttc Val Phe Phe Val Phe Val Val Val Ser Leu Tyr Leu Ser Ala Thr Phe 35 40 45	144
ctc ctc cga tac acc gtc gat tca ctc ccc aca ctc ggt ccc cgc att Leu Leu Arg Tyr Thr Val Asp Ser Leu Pro Thr Leu Gly Pro Arg Ile 50 55 60	192
ctc aaa cca atc aca gcc gtt cac agc ctc att ctc ttc ctc ctc tcc Leu Lys Pro Ile Thr Val His Ser Leu Ile Leu Phe Leu Leu Ser 65 70 75 80	240
tta acc atg gcc gtt ggt tgc act ctc tcc cta atc tct tcc tcg gac Leu Thr Met Ala Val Gly Cys Thr Leu Ser Leu Ile Ser Ser Ser Asp 85 90 95	288
ccg aag gcg cgt ctc ttc gac gcc gtt tgt ttc ccc ctc gac gtg aaa Pro Lys Ala Arg Leu Phe Asp Ala Val Cys Phe Pro Leu Asp Val Lys 100 105 110	336
cct aag gga ccg ctt ttc ttt tgg gct caa gtc ttt tac ctc tcg aag Pro Lys Gly Pro Leu Phe Phe Trp Ala Gln Val Phe Tyr Leu Ser Lys 115 120 125	384
atc ctt gag ttc gta gac aca ctt ctc atc ata ctc aac aaa tca atc Ile Leu Glu Phe Val Asp Thr Leu Leu Ile Ile Leu Asn Lys Ser Ile 130 135 140	432
caa cgg ctc tcg ttc ctc cac gtc tac cac cac gca acg gtt gtg att Gln Arg Leu Ser Phe Leu His Val Tyr His His Ala Thr Val Val Ile 145 150 155 160	480
ttg tgc tac ctc tgg tta cga aca cgt caa tcg atg ttt cct gtt ggg Leu Cys Tyr Leu Trp Leu Arg Thr Arg Gln Ser Met Phe Pro Val Gly 165 170 175	528
ctc gtg ttg aac tcg acg gtc cat gtg att atg tac ggg tac tat ttc Leu Val Leu Asn Ser Thr Val His Val Ile Met Tyr Gly Tyr Tyr Phe 180 185 190	576
ctc tgc gct atc gga tcg agg ccc aag tgg aag aag ttg gtg acg aat Leu Cys Ala Ile Gly Ser Arg Pro Lys Trp Lys Lys Leu Val Thr Asn 195 200 205	624
ttt caa atg gtt cag ttt gct ttc ggc atg ggg tta gga gcc gct tgg Phe Gln Met Val Gln Phe Ala Phe Gly Met Gly Leu Gly Ala Ala Trp 210 215 220	672
atg ctc cca gag cat tat ttc ggg tcg ggt tgc gcc ggg att tgg aca Met Leu Pro Glu His Tyr Phe Gly Ser Gly Cys Ala Gly Ile Trp Thr 225 230 235 240	720
gtt tat ttc aat ggt gtg ttt act gct tct cta ttg gct ctc ttc tac Val Tyr Phe Asn Gly Val Phe Thr Ala Ser Leu Leu Ala Leu Phe Tyr 245 250 255	768
aac ttc cac tcc aag aac tat gag aag act aca acg tcg cct ttg tat Asn Phe His Ser Lys Asn Tyr Glu Lys Thr Thr Thr Ser Pro Leu Tyr 260 265 270	816
aag atc gaa tcc ttt ata ttt att cac gga gag agg tgg gca aat aaa Lys Ile Glu Ser Phe Ile Phe Ile His Gly Glu Arg Trp Ala Asn Lys 275 280 285	864

196

897

gcg att aca tta ttt tcc aag aaa aac gat taa  
 Ala Ile Thr Leu Phe Ser Lys Lys Asn Asp  
 290 295

<210> 136  
 <211> 298  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 136

Met Ala Ser Val Tyr Ser Thr Leu Thr Tyr Trp Leu Val His His Pro  
 1 5 10 15

Tyr Ile Ala Asn Phe Thr Trp Thr Glu Gly Glu Thr Leu Gly Ser Thr  
 20 25 30

Val Phe Phe Val Phe Val Val Val Ser Leu Tyr Leu Ser Ala Thr Phe  
 35 40 45

Leu Leu Arg Tyr Thr Val Asp Ser Leu Pro Thr Leu Gly Pro Arg Ile  
 50 55 60

Leu Lys Pro Ile Thr Ala Val His Ser Leu Ile Leu Phe Leu Leu Ser  
 65 70 75 80

Leu Thr Met Ala Val Gly Cys Thr Leu Ser Leu Ile Ser Ser Ser Asp  
 85 90 95

Pro Lys Ala Arg Leu Phe Asp Ala Val Cys Phe Pro Leu Asp Val Lys  
 100 105 110

Pro Lys Gly Pro Leu Phe Phe Trp Ala Gln Val Phe Tyr Leu Ser Lys  
 115 120 125

Ile Leu Glu Phe Val Asp Thr Leu Leu Ile Ile Leu Asn Lys Ser Ile  
 130 135 140

Gln Arg Leu Ser Phe Leu His Val Tyr His His Ala Thr Val Val Ile  
 145 150 155 160

Leu Cys Tyr Leu Trp Leu Arg Thr Arg Gln Ser Met Phe Pro Val Gly  
 165 170 175

Leu Val Leu Asn Ser Thr Val His Val Ile Met Tyr Gly Tyr Tyr Phe  
 180 185 190

Leu Cys Ala Ile Gly Ser Arg Pro Lys Trp Lys Lys Leu Val Thr Asn  
 195 200 205

Phe Gln Met Val Gln Phe Ala Phe Gly Met Gly Leu Gly Ala Ala Trp  
 210 215 220

## 197

Met Leu Pro Glu His Tyr Phe Gly Ser Gly Cys Ala Gly Ile Trp Thr  
 225 230 235 240

Val Tyr Phe Asn Gly Val Phe Thr Ala Ser Leu Leu Ala Leu Phe Tyr  
 245 250 255

Asn Phe His Ser Lys Asn Tyr Glu Lys Thr Thr Thr Ser Pro Leu Tyr  
 260 265 270

Lys Ile Glu Ser Phe Ile Phe Ile His Gly Glu Arg Trp Ala Asn Lys  
 275 280 285

Ala Ile Thr Leu Phe Ser Lys Lys Asn Asp  
 290 295

<210> 137  
 <211> 837  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1)..(837)  
 <223> Delta-5-Elongase

<400> 137  
 atg gca tca att tac tcc tct tta acc tac tgg ctc gtt aac cac ccc 48  
 Met Ala Ser Ile Tyr Ser Ser Leu Thr Tyr Trp Leu Val Asn His Pro  
 1 5 10 15  
 tac atc tcc aat ttt act tgg atc gaa ggt gaa acc cta ggc tcc acc 96  
 Tyr Ile Ser Asn Phe Thr Trp Ile Glu Gly Glu Thr Leu Gly Ser Thr  
 20 25 30  
 gtc ttt ttc gta tcc gtc gta gtc tcc gtt tac ctc tcc gcc acg ttc 144  
 Val Phe Phe Val Ser Val Val Val Ser Val Tyr Leu Ser Ala Thr Phe  
 35 40 45  
 ctc ctc cga tcc gcc atc gat tca ctc cca tca ctc agt cca cgt atc 192  
 Leu Leu Arg Ser Ala Ile Asp Ser Leu Pro Ser Leu Ser Pro Arg Ile  
 50 55 60  
 ctc aaa ccg atc aca gcc gtc cac agc cta atc ctc tgt ctc ctc tcc 240  
 Leu Lys Pro Ile Thr Ala Val His Ser Leu Ile Leu Cys Leu Leu Ser  
 65 70 75 80  
 tta gtc atg gcc gtc ggt tgc act ctc tca ata acc tca tct cac gcg 288  
 Leu Val Met Ala Val Gly Cys Thr Leu Ser Ile Thr Ser Ser His Ala  
 85 90 95  
 tct tca gat ccg atg gcg cgt ttc ctt cac gcg att tgc ttt ccc gtc 336  
 Ser Ser Asp Pro Met Ala Arg Phe Leu His Ala Ile Cys Phe Pro Val  
 100 105 110  
 gac gtt aaa cct aac gga ccg ctt ttc ttc tgg gct caa gtc ttc tac 384  
 Asp Val Lys Pro Asn Gly Pro Leu Phe Phe Trp Ala Gln Val Phe Tyr  
 115 120 125  
 ctc tcg aag atc ctc gag ttc gga gac acg atc ctc atc ata ctc ggc 432  
 Leu Ser Lys Ile Leu Glu Phe Gly Asp Thr Ile Leu Ile Ile Leu Gly  
 130 135 140

198

aaa tca atc caa cgg cta tcc ttc ctc cac gtg tac cac cac gcg acg 480  
 Lys Ser Ile Gln Arg Leu Ser Phe Leu His Val Tyr His His Ala Thr  
 145 150 155 160  
  
 gtt gtg gtc atg tgt tat ctc tgg ctc cga act cgc caa tcg atg ttt 528  
 Val Val Val Met Cys Tyr Leu Trp Leu Arg Thr Arg Gln Ser Met Phe  
 165 170 175  
  
 ccg att gcg ctc gtg acg aat tcg acg gta cac gtc atc atg tac ggt 576  
 Pro Ile Ala Leu Val Thr Asn Ser Thr Val His Val Ile Met Tyr Gly  
 180 185 190  
  
 tac tac ttc ctc tgc gcc gtt gga tcg agg ccc aag tgg aag aga ttg 624  
 Tyr Tyr Phe Leu Cys Ala Val Gly Ser Arg Pro Lys Trp Lys Arg Leu  
 195 200 205  
  
 gtg acg gat tgt cag att gtt cag ttt gtt ttc agt ttc ggg tta tcc 672  
 Val Thr Asp Cys Gln Ile Val Gln Phe Val Phe Ser Phe Gly Leu Ser  
 210 215 220  
  
 ggt tgg atg ctc cga gag cac tta ttc ggg tcg ggt tgc acc ggg att 720  
 Gly Trp Met Leu Arg Glu His Leu Phe Gly Ser Gly Cys Thr Gly Ile  
 225 230 235 240  
  
 tgg gga tgg tgt ttc aac gct gca ttt aat gct tct ctt ttg gct ctc 768  
 Trp Gly Trp Cys Phe Asn Ala Ala Phe Asn Ala Ser Leu Leu Ala Leu  
 245 250 255  
  
 ttt tcc aac ttc cat tca aag aat tat gtc aag aag cca acg aga gag 816  
 Phe Ser Asn Phe His Ser Lys Asn Tyr Val Lys Lys Pro Thr Arg Glu  
 260 265 270  
  
 gat ggc aaa aaa agc gat tag 837  
 Asp Gly Lys Lys Ser Asp  
 275

<210> 138  
 <211> 278  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 138

Met Ala Ser Ile Tyr Ser Ser Leu Thr Tyr Trp Leu Val Asn His Pro  
 1 5 10 15  
  
 Tyr Ile Ser Asn Phe Thr Trp Ile Glu Gly Glu Thr Leu Gly Ser Thr  
 20 25 30  
  
 Val Phe Phe Val Ser Val Val Val Ser Val Tyr Leu Ser Ala Thr Phe  
 35 40 45  
  
 Leu Leu Arg Ser Ala Ile Asp Ser Leu Pro Ser Leu Ser Pro Arg Ile  
 50 55 60  
  
 Leu Lys Pro Ile Thr Ala Val His Ser Leu Ile Leu Cys Leu Leu Ser  
 65 70 75 80  
  
 Leu Val Met Ala Val Gly Cys Thr Leu Ser Ile Thr Ser Ser His Ala  
 85 90 95

## 199

Ser Ser Asp Pro Met Ala Arg Phe Leu His Ala Ile Cys Phe Pro Val  
 100 105 110

Asp Val Lys Pro Asn Gly Pro Leu Phe Phe Trp Ala Gln Val Phe Tyr  
 115 120 125

Leu Ser Lys Ile Leu Glu Phe Gly Asp Thr Ile Leu Ile Ile Leu Gly  
 130 135 140

Lys Ser Ile Gln Arg Leu Ser Phe Leu His Val Tyr His His Ala Thr  
 145 150 155 160

Val Val Val Met Cys Tyr Leu Trp Leu Arg Thr Arg Gln Ser Met Phe  
 165 170 175

Pro Ile Ala Leu Val Thr Asn Ser Thr Val His Val Ile Met Tyr Gly  
 180 185 190

Tyr Tyr Phe Leu Cys Ala Val Gly Ser Arg Pro Lys Trp Lys Arg Leu  
 195 200 205

Val Thr Asp Cys Gln Ile Val Gln Phe Val Phe Ser Phe Gly Leu Ser  
 210 215 220

Gly Trp Met Leu Arg Glu His Leu Phe Gly Ser Gly Cys Thr Gly Ile  
 225 230 235 240

Trp Gly Trp Cys Phe Asn Ala Ala Phe Asn Ala Ser Leu Leu Ala Leu  
 245 250 255

Phe Ser Asn Phe His Ser Lys Asn Tyr Val Lys Lys Pro Thr Arg Glu  
 260 265 270

Asp Gly Lys Lys Ser Asp  
 275

<210> 139

<211> 6

<212> PRT

<213> Konsensus

<220>

<221> MISC\_FEATURE

<222> (1)..(6)

<223> Xaa in der Position 3 und 4 in der Sequenz hat die in Tabelle A w  
 iedergegebene Bedeutung.

<400> 139

Leu His Xaa Xaa His His  
 1 5

<210> 140

<211> 8

<212> PRT  
<213> Konsensus

<220>  
<221> MISC\_FEATURE  
<222> (1)..(8)  
<223> Xaa an der Position 2, 3, 5 und 6 in der Sequenz hat die in Tabelle A wiedergegebene Bedeutung.

<400> 140

Thr Xaa Xaa Gln Xaa Xaa Gln Phe  
1 5

<210> 141  
<211> 6  
<212> PRT  
<213> Konsensus

<220>  
<221> MISC\_FEATURE  
<222> (1)..(6)  
<223> Xaa an Position 3 in der Sequenz hat die in Tabelle A wiedergegebene Bedeutung.

<400> 141

Asp Thr Xaa Phe Met Val  
1 5

<210> 142  
<211> 8  
<212> PRT  
<213> Konsensus

<220>  
<221> MISC\_FEATURE  
<222> (1)..(8)  
<223> Xaa an Position 5 und 6 in der Sequenz hat die in Tabelle A wiedergegebene Bedeutung.

<400> 142

Thr Gln Ala Gln Xaa Xaa Gln Phe  
1 5

<210> 143  
<211> 60  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(60)  
<223>

<400> 143  
gtcgaccgcg ggaactagtg gccctctaga cccgggggat ccggaatctgc tggctatgaa 60

<210> 144



## 201

<211> 60  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(60)  
<223>

<400> 144  
gtcgcacccgc ggactagtgg gccctctaga cccgggggat ccgcatctgc tggctatgaa 60

<210> 145  
<211> 36  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(36)  
<223>

<400> 145  
ggtaccacat aatgtgcgtg gagacggaaa ataacg 36

<210> 146  
<211> 33  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(33)  
<223>

<400> 146  
ctcgagttac gccgtctttc cggagtgttg gcc 33

<210> 147  
<211> 24  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(24)  
<223>

<400> 147  
gcggccgctt acgtggactt ggtc 24

<210> 148  
<211> 24  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(24)  
<223>

<400> 148  
gcggccgcat ggcgacgaag gagg

24

<210> 149  
<211> 25  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(25)  
<223>

<400> 149  
taagcttaca tggcgacgaa ggagg

25

<210> 150  
<211> 24  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(24)  
<223>

<400> 150  
tggatccact tacgtggact tgggt

24

<210> 151  
<211> 60  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(60)  
<223>

<400> 151  
gtcgaccgcg gcactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa

60

<210> 152  
<211> 31  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(31)  
<223>

<400> 152  
gcggccgcac catgtgctca ccaccgccgt c

31

<210> 153  
<211> 26

<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(26)  
<223>

<400> 153  
gcggccgcct acatggcacc agtaac

26

<210> 154  
<211> 31  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(31)  
<223>

<400> 154  
gcggccgcac catgtgctca tcaccgccgt c

31

<210> 155  
<211> 26  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(26)  
<223>

<400> 155  
gcggccgcct acatggcacc agtaac

26

<210> 156  
<211> 31  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(31)  
<223>

<400> 156  
gcggccgcac catggacgcc tacaacgctg c

31

<210> 157  
<211> 27  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(27)  
<223>

<400> 157  
gcggcgcct aagcactctt cttcttt

27

<210> 158  
<211> 23  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(23)  
<223>

<400> 158  
accatgtgct caccaccgcc gtc

23

<210> 159  
<211> 18  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(18)  
<223>

<400> 159  
ctacatggca ccagtaac

18

<210> 160  
<211> 23  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(23)  
<223>

<400> 160  
accatgtgct catcaccgcc gtc

23

<210> 161  
<211> 18  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(18)  
<223>

<400> 161  
ctacatggca ccagtaac

18

<210> 162  
<211> 23  
<212> DNA

<213> Primer

<220>

<221> misc\_feature

<222> (1)..(23)

<223>

<400> 162

accatggacg cctacaacgc tgc

23

<210> 163

<211> 19

<212> DNA

<213> Primer

<220>

<221> misc\_feature

<222> (1)..(19)

<223>

<400> 163

ctaagcactc ttctttcttt

19

<210> 164

<211> 60

<212> DNA

<213> Primer

<220>

<221> misc\_feature

<222> (1)..(60)

<223>

<400> 164

gtcgaccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa

60

<210> 165

<211> 60

<212> DNA

<213> Primer

<220>

<221> misc\_feature

<222> (1)..(60)

<223>

<400> 165

gtcgaccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa

60

<210> 166

<211> 29

<212> DNA

<213> Primer

<220>

<221> misc\_feature

<222> (1)..(29)

<223>

<400> 166  
gcggccgcat aatgacgagc aacatgagc 29

<210> 167  
<211> 29  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(29)  
<223>

<400> 167  
gcggccgctt aggccgactt ggccttggg 29

<210> 168  
<211> 34  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(34)  
<223>

<400> 168  
gcggccgcac catggacgtc gtcgagcagc aatg 34

<210> 169  
<211> 36  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(36)  
<223>

<400> 169  
gcggccgctt agatggtctt ctgcttcttg ggcgcc 36

<210> 170  
<211> 23  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(23)  
<223>

<400> 170  
gacataatga cgagcaacat gag 23

<210> 171  
<211> 25  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(25)  
<223>

<400> 171  
cggcttaggc cgacttg gcc ttggg

25

<210> 172  
<211> 30  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(30)  
<223>

<400> 172  
agacataatg gacgtcgtcg agcagcaatg

30

<210> 173  
<211> 28  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(28)  
<223>

<400> 173  
ttagatgggc ttctgcttct tgggcgcc

28

<210> 174  
<211> 60  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(60)  
<223>

<400> 174  
gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa

60

<210> 175  
<211> 29  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(29)  
<223>

<400> 175

gcggccgcat aatgggttca acatggcaa

29

<210> 176  
<211> 32  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(32)  
<223>

<400> 176  
gcggccgctt atgtcttctt gctcttcctg tt

32

<210> 177  
<211> 26  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(26)  
<223>

<400> 177  
gcggccgcat aatggagact tttaat

26

<210> 178  
<211> 28  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(28)  
<223>

<400> 178  
gcggccgctc agtccccct cactttcc

28

<210> 179  
<211> 29  
<212> DNA  
<213> Primer

<220>  
<221> misc\_feature  
<222> (1)..(29)  
<223>

<400> 179  
aagcttacat aatgggttca acatggcaa

29

<210> 180  
<211> 30  
<212> DNA  
<213> Primer



<220>  
 <221> misc\_feature  
 <222> (1)..(30)  
 <223>

<400> 180  
 ggatccttat gtcttcttgc tcttcctgtt

30

<210> 181  
 <211> 26  
 <212> DNA  
 <213> Primer

<220>  
 <221> misc\_feature  
 <222> (1)..(26)  
 <223>

<400> 181  
 aagcttacat aatggagact tttaat

26

<210> 182  
 <211> 27  
 <212> DNA  
 <213> Primer

<220>  
 <221> misc\_feature  
 <222> (1)..(27)  
 <223>

<400> 182  
 ggatccttca gtccccctc actttcc

27

<210> 183  
 <211> 993  
 <212> DNA  
 <213> Phaeodactylum tricornutum

<220>  
 <221> CDS  
 <222> (103)..(939)  
 <223> Delta-6-Elongase

<400> 183  
 ggtcttttgt ggtagctatc gtcacacac gcaggctcgtt gctcactatc gtgatccgta

60

tattgaccgt gcacttgtgt aaaacagaga tattttcaaga gt atg atg gta cct  
 Met Met Val Pro  
 1

114

tca agt tat gac gag tat atc gtc atg gtc aac gac ctt ggc gac tct  
 Ser Ser Tyr Asp Glu Tyr Ile Val Met Val Asn Asp Leu Gly Asp Ser  
 5 10 15 20

162

att ctg agc tgg gcc gac cct gat cac tat cgt gga cat acc gag gga  
 Ile Leu Ser Trp Ala Asp Pro Asp His Tyr Arg Gly His Thr Glu Gly  
 25 30 35

210

tgg gag ttc act gac ttt tct gct gct ttt agc att gcc gtc gcg tac  
 Trp Glu Phe Thr Asp Phe Ser Ala Ala Phe Ser Ile Ala Val Ala Tyr

258

## 210

40	45	50	
ctc ctg ttt gtc ttt gtt gga tct ctc att atg agt atg gga gtc ccc Leu Leu Phe Val Phe Val Gly Ser Leu Ile Met Ser Met Gly Val Pro 55 60 65			306
gca att gac cct tat ccg ctc aag ttt gtc tac aat gtt tca cag att Ala Ile Asp Pro Tyr Pro Leu Lys Phe Val Tyr Asn Val Ser Gln Ile 70 75 80			354
atg ctt tgt gct tac atg acc att gaa gcc agt ctt cta gct tat cgt Met Leu Cys Ala Tyr Met Thr Ile Glu Ala Ser Leu Leu Ala Tyr Arg 85 90 95 100			402
aac ggc tac aca ttc tgg cct tgc aac gat tgg gac ttt gaa aag ccg Asn Gly Tyr Thr Phe Trp Pro Cys Asn Asp Trp Asp Phe Glu Lys Pro 105 110 115			450
cct atc gct aag ctc ctc tgg ctc ttt tac gtt tcc aaa att tgg gat Pro Ile Ala Lys Leu Leu Trp Leu Phe Tyr Val Ser Lys Ile Trp Asp 120 125 130			498
ttt tgg gac acc atc ttt att gtt ctc ggg aag aag tgg cgt caa ctt Phe Trp Asp Thr Ile Phe Ile Val Leu Gly Lys Lys Trp Arg Gln Leu 135 140 145			546
tcc ttc ctg cac gtc tac cat cac acc acc atc ttt ctc ttc tac tgg Ser Phe Leu His Val Tyr His His Thr Thr Ile Phe Leu Phe Tyr Trp 150 155 160			594
ttg aat gca cat gta aac ttt gat ggt gat att ttc ctc acc atc gtc Leu Asn Ala His Val Asn Phe Asp Gly Asp Ile Phe Leu Thr Ile Val 165 170 175 180			642
ttg aac ggt ttc atc cac acc gtc atg tac acg tac tac ttc att tgc Leu Asn Gly Phe Ile His Thr Val Met Tyr Thr Tyr Tyr Phe Ile Cys 185 190 195			690
atg cac acc aag gtc cca gag acc ggc aaa tcc ttg ccc att tgg tgg Met His Thr Lys Val Pro Glu Thr Gly Lys Ser Leu Pro Ile Trp Trp 200 205 210			738
aaa tct agt ttg aca agc atg cag ctg gtg cag ttc atc acg atg atg Lys Ser Ser Leu Thr Ser Met Gln Leu Val Gln Phe Ile Thr Met Met 215 220 225			786
acg cag gct atc atg atc ttg tac aag ggc tgt gct gct ccc cat agc Thr Gln Ala Ile Met Ile Leu Tyr Lys Gly Cys Ala Ala Pro His Ser 230 235 240			834
cgg gtg gtg aca tcg tac ttg gtt tac att ttg tcg ctc ttt att ttg Arg Val Val Thr Ser Tyr Leu Val Tyr Ile Leu Ser Leu Phe Ile Leu 245 250 255 260			882
ttc gcc cag ttc ttt gtc agc tca tac ctc aag ccg aag aag aag aag Phe Ala Gln Phe Phe Val Ser Ser Tyr Leu Lys Pro Lys Lys Lys Lys 265 270 275			930
aca gct taa gcgaaatttg ggtctacgtt aaaacaatta cgttacaaaa Thr Ala			979
aaaaaaaaaa aaaa			993

&lt;210&gt; 184

&lt;211&gt; 278

&lt;212&gt; PRT

211

&lt;213&gt; Phaeodactylum tricornutum

&lt;400&gt; 184

Met Met Val Pro Ser Ser Tyr Asp Glu Tyr Ile Val Met Val Asn Asp  
 1 5 10 15

Leu Gly Asp Ser Ile Leu Ser Trp Ala Asp Pro Asp His Tyr Arg Gly  
 20 25 30

His Thr Glu Gly Trp Glu Phe Thr Asp Phe Ser Ala Ala Phe Ser Ile  
 35 40 45

Ala Val Ala Tyr Leu Leu Phe Val Phe Val Gly Ser Leu Ile Met Ser  
 50 55 60

Met Gly Val Pro Ala Ile Asp Pro Tyr Pro Leu Lys Phe Val Tyr Asn  
 65 70 75 80

Val Ser Gln Ile Met Leu Cys Ala Tyr Met Thr Ile Glu Ala Ser Leu  
 85 90 95

Leu Ala Tyr Arg Asn Gly Tyr Thr Phe Trp Pro Cys Asn Asp Trp Asp  
 100 105 110

Phe Glu Lys Pro Pro Ile Ala Lys Leu Leu Trp Leu Phe Tyr Val Ser  
 115 120 125

Lys Ile Trp Asp Phe Trp Asp Thr Ile Phe Ile Val Leu Gly Lys Lys  
 130 135 140

Trp Arg Gln Leu Ser Phe Leu His Val Tyr His His Thr Thr Ile Phe  
 145 150 155 160

Leu Phe Tyr Trp Leu Asn Ala His Val Asn Phe Asp Gly Asp Ile Phe  
 165 170 175

Leu Thr Ile Val Leu Asn Gly Phe Ile His Thr Val Met Tyr Thr Tyr  
 180 185 190

Tyr Phe Ile Cys Met His Thr Lys Val Pro Glu Thr Gly Lys Ser Leu  
 195 200 205

Pro Ile Trp Trp Lys Ser Ser Leu Thr Ser Met Gln Leu Val Gln Phe  
 210 215 220

Ile Thr Met Met Thr Gln Ala Ile Met Ile Leu Tyr Lys Gly Cys Ala  
 225 230 235 240

Ala Pro His Ser Arg Val Val Thr Ser Tyr Leu Val Tyr Ile Leu Ser  
 245 250 255

## 212

Leu Phe Ile Leu Phe Ala Gln Phe Phe Val Ser Ser Tyr Leu Lys Pro  
 260 265 270

Lys Lys Lys Lys Thr Ala  
 275

<210> 185  
 <211> 20  
 <212> DNA  
 <213> Primer

<220>  
 <221> misc\_feature  
 <222> (1)..(20)  
 <223> N in den Positionen 3 und 18 bedeutet C oder T.

<400> 185  
 aactuctut ggctutnta 20

<210> 186  
 <211> 23  
 <212> DNA  
 <213> Primer

<220>  
 <221> misc\_feature  
 <222> (1)..(23)  
 <223> N in den Positionen 3 und 15 bedeutet C oder T. N in den Positionen 9, 12 und 21 bedeutet A oder G.

<400> 186  
 gantguacna anaantgugc naa 23

<210> 187  
 <211> 446  
 <212> DNA  
 <213> PCR-Fragment

<220>  
 <221> misc\_feature  
 <222> (1)..(446)  
 <223> PCR-Fragment

<400> 187  
 aagtcctct ggctctttaa cgtttccaaa atttgggatt tttgggacac catctttatt 60  
 gttctcgga agaagtggcg tcaactttcc ttctgcacg tctaccatca caccaccatc 120  
 tttctcttct actggttgaa tgcacatgta aactttgatg gtgatatttt cctcaccatc 180  
 gtcttgaacg gtttcatcca caccgtcatg tacacgtact acttcatttg catgcacacc 240  
 aaggtcccag agaccggcaa atccttgccc atttgggtga aatctagttt gacaagcatg 300  
 cagctgggtgc agttcatcac gatgatgacg caggctatca tgatcttgta caagggctgt 360  
 gctgctcccc atagccgggt ggtgacatcg tacttggttt acattttgtc gctctttatt 420  
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214

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